

RESULT 11  
 BM690735 675 bp mRNA linear EST 28-FEB-2002  
 Locus  
 DEFINITION UI-E-CKO-aav-c-12-0-UI.r1 UI-E-CKO Homo sapiens cDNA clone  
 UI-E-CKO-aav-c-12-0-UI 5', mRNA sequence.  
 ACCESSION BM690735  
 VERSION  
 SOURCE  
 KEYWORDS  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (Bases 1 to 675)  
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="UI-E-CKO-aav-c-12-0-UI"  
 /tissue\_type="Retina Foveal and Macular"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-CKO"  
 /note="Organ: eye; Vector: pTV73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-E-CKO is a cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."  
 ORIGIN  
 Query Match 17.7%; Score 589.4; DB 12; Length 675;  
 Best Local Similarity 99.7%; Pred. No. 2.1e-120;  
 Matches 601; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 2728 CAAATATAGAGNGTCATGCTTGGCAACAGTAAATCTGAAAGAAAGACACTTACT 2787  
 DB 8 CAAATATAGAGA-TCATGTACTTGGCAACAGTAAATCTGAAAGAAAGACACTTACT 66  
 QY 2788 TATTATTAAACCCCAATGCAATCAGGCAACATATTTTACTATTTCTTGGATCATAGT 2847  
 DB 67 TATTATTAAACCCCAATGCAATCAGGCAACATATTTTACTATTTCTTGGATCATAGT 126

Appendix A

QY 2848 CAAATATGATCATTAAGCCAGGTTTGGTTCCACCTTCCCTGAAAAATTTTACTCAGATCAT 2907  
 DB 127 CAAATATGATCATTAAGCCAGGTTTGGTTCCACCTTCCCTGAAAAATTTTACTCAGATCAT 186  
 QY 2908 TTGCAACAGCATAGCTTACTTATTTGTTAGGAGTGAACAATTTATTGGGAAGCAAACT 2967  
 DB 187 TTGCAACAGCATAGCTTACTTATTTGTTAGGAGTGAACAATTTATTGGGAAGCAAACT 246  
 QY 2968 CTTTATATGCTAGAAAGTACATTTTAAAGATGACTTACGAGGAGATGCGAGGTCTC 3027  
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 QY 3208 AAACGTGAGGTTTCAGATACACATACCATCGGAAAAATCTTTACTTTTCTTGTACTACACAAA 3267  
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 DB 547 GCTATTTTAAAGAGATGCTATGTTGGAGAGGCGGAAGTTGTACTATATGACATAATC 606  
 QY 3328 AAT 3330  
 DB 607 AAT 609  
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 BQ636596 598 bp mRNA linear EST 15-JUL-2002  
 Locus  
 DEFINITION hdlh02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
 Homo sapiens cDNA clone hdlh02 5', mRNA sequence.  
 ACCESSION BQ636596  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 598)  
 AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 TITLE Expressed sequence tag analysis of human retina for the NEIRank Project: retinoidin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts  
 JOURNAL Mol. Vis. 8 (4), 196-204 (2002)  
 MEDLINE 22103461  
 PUBMED 12107411  
 COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 11 row: h column: 02  
 Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers  
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 /clone="hdlh02"  
 FEATURES  
 source

GenCore version 5.1.6  
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Run on: March 1, 2004, 12:42:01 ; Search time 12784 Seconds  
(without alignments)  
11290.074 Million cell updates/sec

Title: US-10-007-270-1  
Perfect score: 3330  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
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- 15: em.ba.\*
- 16: em.fun.\*
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- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
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- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rtd.\*
- 36: em.htg\_nam.\*
- 37: em.htg\_vrt.\*
- 38: em.sv.\*
- 39: em.hgo\_hum.\*
- 40: em.hgo\_mus.\*
- 41: em.hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	3196	96.0	3268	9	AF047492	AF047492 Homo sapi
2	1713.2	51.4	3552	4	AB047844	AB047844 Bos tauru
3	1375.6	41.3	3668	10	AF266478	AF266478 Mus muscu
4	1366.4	41.0	2924	10	BC022970	BC022970 Mus muscu
5	1287.2	38.7	2850	10	AB047843	AB047843 Rattus no
6	1255.2	37.7	3675	10	AF229929	AF229929 Mus muscu
7	823.6	24.7	90766	9	AL392166	AL392166 Human DNA
8	823.6	24.7	132145	2	AL359817	AL359817 Homo sapi
9	814.2	24.5	1235	9	HSIMPG17	AF017776 Homo sapi
10	535.8	16.1	816	9	HSIMPG13	AF017772 Homo sapi
11	535.8	16.1	160719	2	AL157379	AL157379 Homo sapi
12	481.2	14.5	4953	5	AB070714	AB070714 Gallus ga
13	439	13.2	555	9	AF047491	AF047491 Macaca fa
14	282.6	8.5	171412	2	AC120388	AC120388 Mus muscu
15	274.6	8.2	248573	2	AC096467	AC096467 Rattus no
16	249	7.5	444	9	HSIMPG10	AF017769 Homo sapi
17	236.4	7.1	537	9	HSIMPG02	AF017761 Homo sapi
18	236.4	7.1	132145	2	AL359817	AL359817 Homo sapi
19	236.4	7.1	186301	9	AL356962	AL356962 Human DNA
20	226	6.8	448	9	HSIMPG14	AF017773 Homo sapi
21	210.4	6.3	477	9	HSIMPG15	AF017774 Homo sapi
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23	203.4	6.1	3989	9	AF157624	AF157624 Homo sapi
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35	103.2	3.1	227853	2	AC116453	AC116453 Mus muscu
36	103	3.1	1094	9	F271363S12	AF211374 Homo sapi
37	103	3.1	160042	2	AC027757	AC027757 Homo sapi
38	103	3.1	178064	2	AC023311	AC023311 Homo sapi
39	103	3.1	178157	2	AC130436	AC130436 Homo sapi
40	103	3.1	183965	9	AC068764	AC068764 Homo sapi
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44	90	2.7	203971	2	EX649245	EX649245 Danio rer
45	90	2.7	270051	2	EX649488	EX649488 Danio rer

ALIGNMENTS

RESULT 1  
AF047492  
LOCUS  
DEFINITION Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)  
mRNA, complete cds.  
ACCESSION AF047492  
VERSION AF047492  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 3268)  
AUTHORS Kuehn,M.H. and Hageman,G.S.  
TITLE Expression and characterization of the IPM 150 gene (IMPG1)

AF047492 3268 bp mRNA linear PRI 26-OCT-1999  
Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)



Db 1259 ACTGATGAATTCCTGGATCACTGCCAGCCTTTGGTCTGCACACCAATCAGAGCTGCC 1318  
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QY 3061 CTGTAGTGTGTATATGCTCCACACTACGCTCTGATTAACACAAACCTCAGTATTTCAG 3120  
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QY 3241 ATCTTACTTTTGTGTTACTTACACAAAGCTATTTTAAAGAAAGTGTATGTTGGGAGAAG 3300  
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## RESULT 2

AB047844  
LOCUS  
DEFINITION Bos taurus mRNA for MLGAPC core protein, complete cds.  
ACCESSION AB047844  
VERSION AB047844.1  
GI:9955919  
KEYWORDS  
SOURCE Bos taurus (cow)  
ORGANISM  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Bovidae; Bovinae; Bos.  
1 (sites)  
Uehara.F., Ohba.N. and Ozawa.M.  
Isolation and characterization of mucinlike glycoprotein associated  
with photoreceptor cells  
Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)  
20391374  
10937595  
2 (bases 1 to 3552)  
Uehara.F., Ohba.N. and Ozawa.M.  
Direct Submission  
Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University  
Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
Kagoshima 890-8520, Japan  
(E-mail: fuehara@meds.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
Fax:81-99-265-4894)

## FEATURES

Location/Qualifiers  
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## CDS

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## ORIGIN

Query Match 51.4%; Score 1713.2; DB 4; Length 3552;  
Best Local Similarity 75.1%; Pred No. 0;  
Matches 2558; Conservative 0; Mismatches 638; Indels 212; Gaps 25;

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QY 61 TGT--TACTTTTATGAGATTGAGGTGTCTGTGATGTATCAGAAATACCAATGC 118  
DB 83 TGTATATTTTATGAGGTGTGGCTGTCTGGACTATTAICAGAAATATCAATGC 142  
QY 119 ACAAAAGCCAGAGTGTATTGGAAACTAGAGAGCTATTTTGTGTTTGGATTTTCTC 178  
DB 143 ACAAAAGCCAGAGTGCATTGGAGCTGCAAGAGTATTTTTCCTTTGGATTTTCTT 202  
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QY 239 GACAAATCCCCCAAGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAATGTCAACT 298  
DB 263 GATAATGCCCGAGACTGAGCAACCAAAATACCGCAAAACGTACAAAGTGTCAACC 322  
QY 299 ATGAGACGAATATTCGATTGGCAAGCATCGAACCAAAAGATCCGCAATTTTCCCAAG 358  
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QY 419 TATAGATTGAGAGTGTGTGAGGAAGCAGTATGGAAGCATATCGGATCTTTCTGATCGC 478  
DB 443 TATAGATTGAGAGTGTGTGAGGAAGCGGTGTGGAAGCTTACCGATCTTTCTGATCGC 502  
QY 479 ATCCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCGACAGAGACCTTTCG 538  
DB 503 CTCCTTGAGCCCGGGGAATACCAAGACTGGGTGAGCATCTGCGACAGAGACCTTTCG 562  
QY 539 CTCCTTTGACATTTGAAAAAATCTTCAAGCAATTCAGGAGCAGCTGGAATCTTCTCAGCAG 598  
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QY 659 GGAGAGCCTGGTGAACCAATTCATTTCAACAGCAATCTACATTTCAAGAGACTTGGGCA 718  
DB 683 GGAGAGCTTGGTCAAAACCCCTGCTCTTCAA----- 712  
QY 719 GTATTCTAAGAAAAACCTCAGAAGAGCAAAATTCAGAGTGTTCCTCAAGCTCTCATTGGGC 778  
DB 713 -----CAGACGTTGCCAGTGTCTCACCGGCG 739  
QY 779 CTTTCCTCTCACTCCTGTGATGACCCCTCTCAATGAATTTCCGATATACATCAACG 838  
DB 740 CTTGTGCTCTCCCTACCGATGAC-CAGTCTCAAGAAATCTCACTACCCCTTCCCG 798  
QY 839 --ACACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTGTGG----- 886  
DB 799 GACACCCAGAGTGCCTTACAGAGAAAGAAATAGAAATTCATGTGCTGTGAGGATGC 858  
QY 887 --AGGAGCAGAGGTGGAGCTCAGGTCTCTCTGTGAACAGAGATTCAGAGCAGAGCT 944  
DB 859 ACTGGAGCAGAAAGTAGAGTAAGTATCTCTGCGCAACCCAGAAAGTTCAGGTCAAGCT 918  
QY 945 CGCTGACTCCAGTCCCTCATATTTACCAGGAGCTAGCAGGAAAGTCCCAACTTTCAGATGCA 1004  
DB 919 GGATACTCCAGTCCCGGTATTTACTCTGAGGTGCGAGCCAGTCTCAGCTTCAGATGCA 978  
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Db 1399 ACTTCTCTTGGTCAACCGAGCTGGAGACAGTGGACAGAGACAGACAGTCCACCTGG 1458  
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Db 1816 CTTGAGAACATCACTCTCTGACCCAGGTTGGCTACATCAACCCAGCGCATGACTGT 1875  
Qy 1890 TGCCCCAAGGCGAGAGCTGGTAGTCTTCTCAGTCTGGGTGTCATACTGAGCTT 1949  
Db 1876 CGCTCCAGGCGCGAGAGTGGTGGTCTTCTCAGTCTGGGTGGCCATGTCGCTT 1935  
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Db 2116 ATATACCTCACAGGCTGTGCAAGGCTCTTGAGGATTTTCTGCTGTCAGGCCA 2175  
Qy 2190 ACACTCCATCTGGAATPAGACAGTACTCTCTCAACATTGAACAGCTGATCAAGCAGA 2249  
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Db 2296 GGAAGCGAGTGTCTGCTCGATCGGA-----A 2324  
Qy 2370 ACCAGGCTCTGTGGCCCTCGGACAAAGGAATGGAGTCTCTCCAGGAAAGGAGCTCC 2429  
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Db 2563 ACCTAATCTATCTCAAGAGAATGATTTCTTTCTCAAGAAAATTTGAATTTCACTCTCT 2622  
Qy 2648 -----GAAAATGGAGACAGGCATATTCATGGGTCTATCAAAATCCAGACATACAGTC 2698  
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Qy 2759 AGTAAATTTCTGAAAAAAAAGACACTTACTTATTTAAACCCCAAAATGCAATCAGCGAA 2818  
Db 2742 AATAAATTTCTGAAGAAAAG-----CAGCTTATATCAAAACCCAAACACATCAGTGAA 2797  
Qy 2819 AC-----ATATTTTACTATCTTTGGATGATAGTCAAAATGATCAAGCCAGTTTG 2871  
Db 2798 ACATAGTAAATATTTTGGTTATTTCTCAGTCAGTCAGGTGATGCAAAACCCAGTTT 2857  
Qy 2872 CTTCCACCTTCCCTGAAAAATTTTACTCAGATCATTTTCAACAAAGCATAGCTTACTT-- 2929  
Db 2858 TGTCTAGCTGCCCTTAAATATTTGCTCAGATCATTTACAAAGTGCATTTATTTGG 2917  
Qy 2930 ----ATGTTTGGGACTGAAACAATTTATTTGGGAAGCAAACTCTTTATATGCTAGAAAT 2985  
Db 2918 GGGCAGGCGGTGGGATTCACCATATACCAAGAAATAAAGCTCTTCACATGTTAGGATGT 2977  
Qy 2986 ACATTTAAAGATGACTACTTACGAGGAGATGAGGTCTCTCTAAACGCGATGATGTA 3045  
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Db 3020 --TAAGGACATGAACTGTGGTGAGCACATAGGTGCTCCACACTTC-AGTGTCTGTAATC 3076  
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Qy 3226 ACATACCATGG-AAAAATCTTACTTTCTGTTTACTACACAAAGCTATTTTAAAGAAAT 3284  
Db 3190 ACATATGATGGAAAAATCTTACTTTCTTGTGTAAGTGTGATGATGATGATTTTGAAGAA 3249  
Qy 3285 GCTATGTT--GGGAGAGGGCGAAGTGTGATCTATATGATCAATCAAT 3330  
Db 3250 TATATATCGGGAAAAAAGTGGGTTGACTTTGTGACATTAACCAAT 3297

## RESULT 3

AF266478

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF266478 3668 bp mRNA linear ROD 18-AUG-2000  
Mus musculus IPM 150 proteoglycan mRNA, complete cds.

AF266478.1 GI:9844921

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3668)

Kuehn, M.H., Wietacki, D.T. and Hageman, G.S.

Molecular characterization of the murine orthologue of the human

retinal proteoglycan IPM 150  
Mol. Vis. 6 (2000) In press  
2 (bases 1 to 3668)  
Kuehn, M.H., Wietacki, D.T. and Hageman, G.S.  
Direct Submission  
Submitted (10-MAY-2000) Ophthalmology, University of Iowa, 2501  
Crosspark Rd., Coralville, IA 52241, USA  
Location/Qualifiers  
1..3668  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
136..2392  
/codon\_start=1  
/product="IPM 150 proteoglycan"  
/protein\_id="AA000796.1"  
/db\_xref="GI:984922"  
/translation="MNFGIKHAFVFGIFLOVQGIKDSIKIFSEIKNIDKPRIET  
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SPGRKDETASMETLEATEAVPTDYSRMSLGFPLPSDDTLKELSLVLDLQK  
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FKLPGFGRVIRVLGFRPKBEDSGSSIEIQLMIAIKRDHAEKSPDLSLSDNKIE  
SERIHGVIEDQPTLYLTATDLKKLIIQLLDGLSLVGEKIPFGEVETGLFRPVE  
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"

Query Match 41.3%; Score 1375.6; DB 10; Length 3668;  
Best Local Similarity 70.7%; Pred. No. 0;  
Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATAATTAATTTTCAATTTT 60  
DB 62 TAAACCAAGGAGTCTGTCTACTCAGCGGCACCTGGATTGATTATTTTCAATTTT 121  
QY 61 TGTATCTTTT-----AATGAGATTGAGGTGTCTGTGATGTCTATCAGATTACC 113  
DB 122 AGTCACCTTATTTCTTTAAGTGTGACTTGGTATTTGTCTGTGATTTT--TCAGATTACC 179  
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QY 174 TTCTCCAAGTTCAAGGAACCAAGATATCTCCATTAAACATATACCATTCGAACTAAAG 233  
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DB 716 CACTGGAAGCAGCCTACTGGAAGCCCTGTGTGTACCCAC----- 752  
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DB 1014 GCAAAAGATATTTAAGAAATCTCCAGGATTCGGAGAAATCCGTGTATTAGGATTTAGACC 1073  
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Db 1902 CATTGCCACCAAGGCGGAGAGCTAGTGGTATCTTTCAGCCCTGGGTGTGCTAACATGCC 1961  
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QY 2999 GACTACTTACGC 3010  
Db 3015 TATCATTTGGGC 3026

## RESULT 4

BC022970

LOCUS

DEFINITION

Mus musculus interphotoreceptor matrix proteoglycan 1, mRNA (cdna

clone MSC:35847 IMAGE:5366008), complete cds.

ACCESSION

BC022970

VERSION

BC022970.1

KEYWORDS

MGC.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2924)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stableton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Schetz,T.E., Brownstein,M.J., Udén,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullen,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahy,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smillius,D.E.,

Schurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED

12477932

REFERENCE

2 (bases 1 to 2924)

Strausberg,R.

Direct Submission

Submitted (04-FEB-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk



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## RESULT 5

AB047843

LOCUS

DEFINITION

AB047843

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

AB047843 2850 bp mRNA linear ROD 30-AUG-2000  
Rattus norvegicus mRNA for MLGAPC core protein, complete cds.

AB047843.1 GI:9955917

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (sites)

Uehara,F., Ohba,N. and Ozawa,M.

Core Protein of rat Mucinlike Glycoprotein Associated with

Photoreceptor Cells

Published Only in DataBase (2000)

2 (bases 1 to 2850)

Uehara,F., Ohba,N. and Ozawa,M.

Direct Submission

Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University

Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,

Kagoshima 890-8520, Japan

(E-mail:fuehara@med5.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,

Fax:81-99-265-4894)





QY 1690 CQTGCATCTTCAGATGACAG-----CCGATCAAGTGCAGGTGGCGAAGATATGGTCAGACAC 1746  
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## RESULT 6

AF229929

LOCUS

DEFINITION

Mus musculus sialoprotein associated with cones and rods SPACR

ACCESSION

AF229929

VERSION

AF229929.1

KEYWORDS

3675 bp mRNA linear ROD 15-NOV-2000  
 Mus musculus sialoprotein associated with cones and rods SPACR  
 mRNA, complete cds.  
 AF229929.1 GI:11177167

SOURCE  
ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 3675)

Lee, J.W., Chen, Q., Rayborn, M.E., Shadrach, K.G., Crabb, J.W.,

Rodriguez, I.R. and Hollyfield, J.G.

SPACR in the interphotoreceptor matrix of the mouse retina:

molecular and biochemical characterization

Unpublished

2 (bases 1 to 3675)

Rodriguez, I.R., Lee, J.W. and Hollyfield, J.G.

Direct Submission

Submitted (31-JAN-2000) LRCMB, NEI-NIH, 6 Center Drive MSC2740

6/304, Bethesda, MD 20892, USA

Location/Qualifiers

1. 3675

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interphotoreceptor matrix"

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SPACR"

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## ORIGIN

Query Match

Best Local Similarity 37.7%; Score 1255.2; DB 10; Length 3675;

Matches 2007; Conservative 69.0%; Pred. No. 4.5e-293;

Mismatches 746; Indels 155; Gaps 15;

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QY 214 ATACCATCTGAAACTAAAGACATAGACAATCCCCAAGAAATGAAACAACCTGAAGATAC 273

Db 144 ATGCTATCTTTGTTTGGGATTTTCTCCAGTTCAGGAATCAACAATTCGAAGTAC 203

QY 274 TGAATAATGTACAAATGTCAACTATGAGACGAATATTCGATTTGGGAAAGCATGCAAC 333

Db 204 TTCAACAGTGCACAAAGTGTCAACCATGAAGCAATATTCGATTTGCCAAAGCTTCAAC 263

QY 334 AAAAGATCGCATTTTTCCTCCACGGGGTAAAGTCTGCACAGGAATCCATGAACA 393

Db 264 CAAAAGATAGCACTTTTCCCA---GCTCTAACATCTGTCCCAGGAATCTTGGACA 320

QY 394 GATTTTAGACAGTCTTCAAGCTTATATAGATTGAGAGTGTGTCAAGGAAGCAGTATGGGA 453

Db 321 GATTTTAGCAAGTCTTCAAGAAATATATAGACTGAGAGTATGTCAAGAAAGTCTGTGGGA 380

QY 454 AGCATATCGATCTTTTCTGGATCGCATCCCTGACACAGGGAATATCAGACTGGGTGAG 513

Db 381 AGCATATCGTATCTTTCTGGACCGAATCTCTGACACAGAGGAATATCAAGACTGGGTGAG 440

QY 514 CATCTGCACGACGAGACCTTCTGCTCTTTTGACATTTGGAAAAAACTTCAGCAATTTCCA 573



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Qy	1747	CTAGATGAATGGATCTGTCTGCACACTCTCGCCCCAATCTGAGGTACACAGAGCTCAGCGAA	1806
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Db	1747	ATCACCAACAGCTCCGAGACCAATTTGCCCAAGGCCGAGAGCTAGTGTATTTCTTCAGC	1806
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Db	1807	CTGGGTGTTGCTTAACATGAGCTTTCTCCATGACCTGTTCACCAAGAGTTCTCTGGAGTAT	1866
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## RESULT 8

AL359817 LOCUS  
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 VERSION AL359817.6 GI:12225447  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_CANCELLED.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

1. McLay, K.

Direct Submission  
 Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk

## COMMENT

On Jan 14, 2001 this sequence version replaced gi:12214326.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bA505B21

----- Summary Statistics

Assembly program: XGAP4, version 4.5

Sequencing vector: plasmid; 108752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 117761 bases at least Q40

Consensus quality: 123343 bases at least Q30

Consensus quality: 126505 bases at least Q20

Insert size: 125645; sum-of-contigs

Insert size: 168195; 8.3% error; agarose-fp

Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality

coverage: 2.65x in Q20 bases; agarose-fp

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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 26 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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 \* 9013: gap of 100 bp  
 \* 12665: contig of 3653 bp in length  
 \* 12666: gap of 100 bp  
 \* 12766: 16825: contig of 4060 bp in length  
 \* 16826: 16925: gap of 100 bp  
 \* 16926: 22958: contig of 6033 bp in length  
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 \* 23059: 23058: contig of 2022 bp in length  
 \* 25081: gap of 100 bp  
 \* 25180: 27272: contig of 2092 bp in length  
 \* 27273: gap of 100 bp  
 \* 27373: 40754: contig of 13382 bp in length  
 \* 40755: 40854: gap of 100 bp  
 \* 40855: 45147: contig of 4293 bp in length  
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\* 62846 70684: contig of 7839 bp in length  
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## FEATURES

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DEFINITION	complete cds.		
ACCESSION	AF017776.1	GI:3800731	
VERSION			
KEYWORDS			
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DB 381 TTCTTAAGTCTTAAAGATTTCTCTTTCAGGTAATCAGTAAAGAAATCTCAATAC 440

QY 2537 TGACCGTAGAATATGAAGAAATTAACCATCAAGATTGGGAAGGAAATTAAGAACTGAAA 2596
DB 441 TGACCGTAGAATATGAAGAAATTAACCATCAAGATTGGGAAGGAAATTAAGAACTGAAA 500

QY 2597 TGTAACATATCACTAGGCTATCTCAGAGAGATGATTTCCTTCCTCAAGGAAATGGA 2656
DB 501 TGTAACATATCACTAGGCTATCTCAGAGAGATGATTTCCTTCCTCAAGGAAATGGA 560

QY 2657 GACAGGCATATTCATGGGTCTCAAAATCCAGACATACAGTCAACACTGAGAATCAGCAC 2716
DB 561 GACAGGCATATTCATGGGTCTCAAAATCCAGACATACAGTCAACACTGAGAATCAGCAC 620

QY 2717 ACACCATATTTCAATATAGAGAGTCAATGCTTTGGCAACAGTAAATTCGAA-AAAA 2775
DB 621 ACACCATATTTCAATATAGAGAGTCAATGCTTTGGCAACAGTAAATTCGAGAAAA 680

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DEFINITION AF017772
ACCESSION AF017772.1 GI:3800727
VERSION
KEYWORDS
SEGMENT 13 of 17
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 816)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Zelbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
JOURNAL 98358139
MEDLINE PUBMED
REFERENCE 2 (bases 1 to 816)
AUTHORS Gehrig,A., Zelbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.B.
and Weber,B.H.F.
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bifocal choriorretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRL)
Unpublished
JOURNAL 3 (bases 1 to 816)
REFERENCE 3 (bases 1 to 816)
AUTHORS Zelbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
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Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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## RESULT 11

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VERSION AL157379.14 GI:15590763
KEYWORDS HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE Homo sapiens
ORGANISM Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

## REFERENCE

```
1
Wall M.
Direct Submission
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 12, 2001 this sequence version replaced gi:11991356.
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## COMMENT

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----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
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Center project name: dj62L18  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 160382 bases at least Q40  
Consensus quality: 160493 bases at least Q30  
Consensus quality: 160578 bases at least Q20  
Insert size: 160719; sum-of-contigs  
Insert size: 158939; 9.3% error; agarose-fp  
Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
coverage: 8.41x in Q20 bases; agarose-fp

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\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

## FEATURES

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## ORIGIN

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Query Match      16.1%; Score 535.8; DB 2; Length 160719;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1481 CTGACATCTTTGGTCTCCACCTGTATGGCTCTACTCCCTGTCAGAAAGCTCCACCTT 1540
Db 7764 CAGACATCTTTGGTCTCCACCTGTATGGCTCTACTCCCTGTCAGAAAGCTCCACCTT 7705
QY 1541 TCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGACCAACAGATCAATGGCCA 1600
Db 7704 TCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGACCAACAGATCAATGGCCA 7645
QY 1601 CTGACCAAGATCTGTAGTACAGGGCTCAACATCCCAACAGTGAATTTCTGCAATCA 1660
Db 7644 CTGACCAAGATCTGTAGTACAGGGCTCAACATCCCAACAGTGAATTTCTGCAATCA 7585
QY 1661 GCCAATGGCTCTGGGAATTTCCATCCACCTGCTATCTTCAGATGACAGCCGATCAAGTG 1720
Db 7584 GCCAATGGCTCTGGGAATTTCCATCCACCTGCTATCTTCAGATGACAGCCGATCAAGTG 7525
QY 1721 CAGTGGCAAGATATGTCAGACACCTAGATGAATGATCTGTGACACTCTCTGCC 1780
Db 7524 CAGTGGCAAGATATGTCAGACACCTAGATGAATGATCTGTGACACTCTCTGCC 7465
QY 1781 CATCTGAGGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGGATA 1840
Db 7464 CATCTGAGGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGGATA 7405
QY 1841 CCACTCTCTCTCAGCTTTTACAGTATATCAACACTAGTTCTATGACCAATTTGCCCCCAAG 1900
Db 7404 CCACTCTCTCTCAGCTTTTACAGTATATCAACACTAGTTCTATGACCAATTTGCCCCCAAG 7345
QY 1901 GCCGAGAGCTGGTGGTGTCTTTCAGTCTGGTGTGCTTAACATGGCTTCTTCAACAGACC 1960
Db 7344 GCCGAGAGCTGGTGGTGTCTTTCAGTCTGGTGTGCTTAACATGGCTTCTTCAACAGACC 7285
QY 1961 TGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCTGGTG 2019
Db 7284 TGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCTGGTG 7226
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QY 1179 AATTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGACAGCACAGAAATCTA 1238
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QY 1239 TCTCAGAGCTTACAGACCTCAAAAGGCTGTATCAGCAAGCACTAGAGGAAGA-----ACA 1292
Db 1269 ACTCAGAGTAACAGACCTTCAGCAGCTGGTGGCCACAGCACTCCATGAAGACAGATCCCT 1328
QY 1293 ATCTTTGGATGGGAGCAATTCAGTTCACTGATGAATTTGCTGATCACTGCCAGCCTT 1352
Db 1329 ACCAGTGGACCTTTGGGACACTTCGGTTTACTGACGAACCTATTAAACCACTCAAGTGATT 1388
QY 1353 TGTCTCTGACACCAATCAGAGCTGCCACATCTTTGCTGTATTAACAGAGAGTGCTAC 1412
Db 1389 TGATAATGACATCAAGGCATGTCTACTTCTCTGGCAGGCCCTGATTGGATGACAC 1448
QY 1413 TTTGAGTCCAGAACTCTCTCTCTGAAACCCAGCTTGAGACAGTGGAGCGAGC 1466
Db 1449 CATAAGCGCAGAACTCCCACTGGTTTATCCAGCCCAATAACAGTGGACCAAC 1502

RESULT 13
AF047491
LOCUS
DEFINITION
Macaca fascicularis interphotoreceptor matrix proteoglycan 150
mRNA, partial cds.
ACCESSION
AF047491
VERSION
AF047491.1 GI:2906229
KEYWORDS
Macaca fascicularis (crab-eating macaque)
SOURCE
Macaca fascicularis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE
1 (bases 1 to 555)
Kuehn, M.H. and Hageman, G.S.
Characterization And Complete cDNA Sequence Of IPM 150, A Novel
Human Photoreceptor Cell-Associated Chondroitin-Sulfate
Proteoglycan
Unpublished
REFERENCE
2 (bases 1 to 555)
Kuehn, M.H. and Hageman, G.S.
Direct Submission
Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City, IA
52240, USA
FEATURES
Location/Qualifiers
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/db_xref="taxon:9541"
/tissue_type="retina"
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/protein_id="AAC03788.1"

CDS
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RIPDTGEYQDWSFCQQTFCFLFDIGQNFNSQEHLDLQQRKQSFPERDEVSTE
KITGESEITVSTDVASVSLGPPVPTPDTLLNELDNLALDKMPTTERETELAS
EEQRVELSISLINQRFKAEALDSQS"

ORIGIN
Query Match 13.2%; Score 439; DB 9; Length 555;
Best Local Similarity 85.8%; Pred. No. 3e-95;
Matches 526; Conservative 0; Mismatches 25; Indels 62; Gaps 1;

QY 347 TTTTTCACAGGGGGTTAAAGTCTGTCACAGGAATCCATGAACAGAGATTTAGACAGT 406
Db 4 TTTTTCGACAGGGGGTTAAAGTCTGTCACAGGAATCCATGAACAGAGATTTAGCCAGT 53

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QY 407 CTTCAAGCTTATTATAGATTGAGAGTGTGTGTCAGGAAGCAGTATGGGAAGCATATCGGATC 466
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QY 467 TTTCTGGATCCGATCCCTGTCAGCAGGGGAATATCAGGACTGGGTGTCAGCATCTCCAGCAG 526
Db 124 TTTCTGGATCCGATCCCTGTCAGCAGGGGAATATCAGGACTGGGTGTCAGCATCTCCAGCAG 183
QY 527 GAGACCTCTTCCTCTTGGACATTGGAAAAAATTCAGCAATTCGCCAGGAGCAGCCTGGAT 586
Db 184 GAGACCTCTTCCTCTTGGACATCGGACAAAATTCAGCAATTCGCCAGGAGCAGCCTGGAT 243
QY 587 CTTCTCCAGCAGAGAAATAAAACAGAGAAAGTTTCCCTGACAGAAAAAGATGAATATCTGCA 646
Db 244 CTTCTCCAGCAGAGAAATAAAACAGAGAAAGTTTCCCTGACAGAAAAAGATGAATATCTACA 303
QY 647 GAGAGACATTTGGAGAGCCTGGTGAACCATTTGTCATTTCAACGCAATCTACATTTCA 706
Db 304 GAGAAGACATTTGGAGAGCCTGTGTAACCATTTGTGTTTCAAC----- 347
QY 707 AAGACTTTGGGCAGTATTCTTAAGAAAAACCTTCAGAGAGCAAAATTCAGAGTTTGCCAAAG 766
Db 348 -----AGATGTTGCCAGCG 361
QY 767 TCTCACTTGGGCCTTTCCCTCTCCTCCTGATGACACCCCTCCTCAATGAATTCGATA 826
Db 362 TCTCACTTGGGCCTTTCCCTCTCCTCCTGATGACACCCCTCCTCAATGAATTCGATA 421
QY 827 ATACACTCAACGACACCAAGATGCTTACACAGAAAAAGAGAAATTCGCTGTGTGG 886
Db 422 ATGCACTCAACGACACCAAGATGCTTACACAGAAAAAGAGAAATTCGCTGTGTGG 481
QY 887 AGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGTAACCAAGAGTTCAAGGAGAGCTCG 946
Db 482 AGGAGCAGAGGGTGGAGCTCAGCATCTCTCTGTAACCAAGAGTTCAAGGAGAGCTCG 541
QY 947 CTGACTCCAGTC 959
Db 542 CTGACTCTCAGTC 554

RESULT 14
AC120388
LOCUS
DEFINITION
Mus musculus chromosome 9 clone RP24-300P2 map 9, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
ACCESSION
AC120388.4 GI:39930692
VERSION
HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 171412)
Birren, B., Nussbaum, C. and Lander, E.
Mus musculus chromosome 9, clone RP24-300P2
Unpublished
REFERENCE
2 (bases 1 to 171412)
Birren, B., Linton, J., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gordon, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, J., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Lakocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunhkhong, P., Pierre, N., Pollara, V.,

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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshekwa, L., Louleghed, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M.P., McNeill, F.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidas, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeleneh, O., Okwuonu, G., Olarnpunsuagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Rades, R., Rachein, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, I., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, D., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wood, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

## TITLE

JOURNAL

REFERENCE

2 (bases 1 to 248573)

Worley, K.C.

Direct Submission

JOURNAL

TITLE

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 248573)

Rat Genome Sequencing Consortium.

Direct Submission

JOURNAL

TITLE

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:23264514.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature

table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GPCR

Center clone name: CH230-85A18

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 236654 bases at least Q40

Consensus quality: 238781 bases at least Q30

Consensus quality: 240212 bases at least Q20

Estimated insert size: 249458; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length

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\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 2 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 247402: contig of 247402 bp in length

\* 247502: gap of unknown length

\* 247503 248573: contig of 1071 bp in length.

## FEATURES

Location/Qualifiers

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/db\_xref="taxon:10116"

/clones="CH230-85A18"

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95023..95328

/note="clone boundary"

clone end:Sp6

site:ECORI

end\_sequence:BH302192"

misc\_feature

misc\_feature

ORIGIN

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Best Local Similarity 70.8%; Pred. No. 3e-55;

Matches 380; Conservative 0; Mismatches 154; Indels 1;

QY 1483 GACACTCTTGGCTCTCCACCTGCTATGGCTCTACCTCCCTGTGAGAGTCCACCTTTC 1542

Db 213183 GACAGTCTTGGCTCTGCTGTGAGAGTCCAGCTCGACTTCGGAGTGGGAATCTACCTTC 213124

QY 1543 TTTATGGATCAAGCATCTTCTCTGACTGATCAAGGACCAACAGATCAATGGCCACT 1602

Db 213123 TTTACGCT--AGCATCTTGGCTCTGAGATCAAAAGCTCCCTCCCTTGTATGGCCACT 213067

QY 1603 GACCAGCAATGCTAGTACAGAGGCTCCACCTCCACCTGATGATTTCTGCAATCAGC 1662

Db 213066 GGCACACAGATTCATCCCAAGCTCACTCTCCCACTCTCGATTTCTACCGTCCGC 213007

QY 1663 CAATGGCTCTGGGAATTTCAATCCACTCTCATCTTTCAGATGACAGCGATCAAGTGCA 1722

Db 213006 CAATGGCGCTAGAGTGTCAATTTGGCTGAGTCTTCCAGTGACAGAGATTGACCACA 212947

QY 1723 GGTGGCAGATATGTTGTCAGACACCTAGTAAATGATCTGTCGACACTCTCCGCCCA 1782

Db 212946 AGCAGCCACGACACAATCAGAGACCTAGATGAATGATGTCCGACACGCTGCTTG 212887

QY 1783 TCTGAGGTACAGAGCTCAGCGAATATGTTTCTCTCCAGATCATTTCTTGGAGGATACC 1842

Db 212886 TCGGAATAGCAGAACTGAGTGGATATGACTCTCCCGGATCGGTTTGGAGATGACC 212827

QY 1843 ACTCTGTCTGCTTACAGTATATCACCACCTAGTTCTATGACCATTCGCCCAAGGC 1902

Db 212826 ACGCCATCCCGACATACAGTATGTCAACACCTAGCTGAGACATTCGCCCAAGGC 212767

QY 1903 CGAGAGCTGGTAGTGTCTTCTCAGTCTGGTGTGTAACATGGCTTCTCCAGAGCTG 1962

Db 212766 CACGAGCTAGTGTATTTCTTCTGAGTCTGGCGTCTGATGCTGCTCTCTATGACTTG 212707

QY 1963 TTCAACAGAGCTCTCTGGAGTACCGAGCTCTGAGGACAAATTCACACAGCTGCTG 2019

Db 212706 TTCAATAGAGTTCCCTGGAGTACCAAGCTTGAACACAGATTCACAGAGCTGCTG 212650

Search completed: March 1, 2004, 18:13:25

Job time : 12825 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 14:08:16 ; Search time 8150 Seconds  
(without alignments)

12201.357 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaaccaagaaggttatcct.....tactatatgacataatcaat 3330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_esti:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est6:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pig:\*

27: em\_gss\_vri:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1642.4	49.3	1665	29 AY415971	AY415971 Homo sapi
2	943.6	28.3	1647	29 AY415973	AY415973 Mus muscu
3	739.2	22.2	1587	29 AY415972	AY415972 Pan trogl
4	716.2	21.5	801	12 BG196799	BG196799 RST16026

5	640.2	19.2	836	12	BI752112	BI752112 603022362
6	634	19.0	690	13	EX510244	EX510244 DXF2p866P
7	628.8	18.9	633	12	BM695987	BM695987 UI-E-CL1-
8	626	18.8	626	13	BQ639265	BQ639265 hd33d04.Y
9	617.2	18.5	622	13	BQ638902	BQ638902 hd329a06.Y
10	615.6	18.5	653	12	BM685921	BM685921 UI-E-CKO-
11	589.4	17.7	675	12	BM690735	BM690735 UI-E-CKO-
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13	498.4	15.0	508	14	CA333958	CA333958 cs44g04.Y
14	472	14.2	472	13	EX097138	EX097138 EX097138
15	459.6	13.8	561	14	W26960	W26960 16h10 Human
16	442.2	13.3	698	13	BU729227	BU729227 UI-E-CL1-
17	433	13.0	683	13	BU732814	BU732814 UI-E-CQ1-
18	429.6	12.9	824	12	BI738733	BI738733 603358767
19	418.2	12.6	963	13	BU506195	BU506195 AGENCOURT
20	409	12.3	422	12	BM726533	BM726533 UI-E-EJO-
21	386	11.6	448	12	BM681190	BM681190 UI-E-EJO-
22	385.6	11.6	851	12	BI733865	BI733865 603353151
23	380.2	11.4	393	13	BQ636351	BQ636351 hd07h06.Y
24	376.2	11.3	641	13	BU734170	BU734170 UI-E-CK1-
25	363.2	10.9	368	12	BM694699	BM694699 UI-E-CI1-
26	354.4	10.6	405	14	H38604	H38604 YD48e04.r1
27	327	9.8	510	9	AL713229	AL713229 DXF2p866P
28	323	9.7	618	14	CA391789	CA391789 cs18h07.Y
29	317	9.5	322	9	AA326863	AA326863 EST30113
30	298.8	9.0	309	14	H38594	H38594 YD48c06.r1
31	298.2	9.0	701	29	AG128736	AG128736 Pan trogl
32	292.4	8.8	797	11	AK020862	AK020862 Mus muscu
33	291	8.7	298	9	AA296278	AA296278 EST10795
34	282.4	8.5	521	12	BM691879	BM691879 UI-E-CL1-
35	282.4	8.5	548	13	BU728582	BU728582 UI-E-CL1-
36	274.4	8.2	340	9	AV656968	AV656968 AV656968
37	271	8.1	753	12	BI735383	BI735383 603356869
38	268	8.0	515	13	BU726282	BU726282 UI-E-CKO-
39	262	7.9	527	13	BU731220	BU731220 UI-E-CI1-
40	262	7.9	567	28	AZ974344	AZ974344 2M0243F20
41	253.2	7.6	886	14	CF549501	CF549501 AGENCOURT
42	238	7.1	802	12	BI735091	BI735091 603356230
43	226.2	6.8	678	28	AZ876525	AZ876525 2M0191104
44	224.2	6.7	813	13	EX743512	EX743512 BX743512
45	222.4	6.7	481	9	AI510373	AI510373 mp95e12.Y

## ALIGNMENTS

RESULT 1	AY415971	1665 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY415971	1665 bp	DNA	linear	GSS 17-DEC-2003
DEFINITION	Homo sapiens IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY415971				
VERSION	AY415971.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trices				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1665)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				



Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.B. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

# JOURNAL PUBMED REFERENCE AUTHORS

2 (bases 1 to 1647)  
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Fanenbaum, D.M., Givello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.B. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

# JOURNAL

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment

# FEATURES

source  
location/Qualifiers  
1..1647  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
1..1647  
/gene="IMPG1"  
/locus\_tag="HMC5735"

# ORIGIN

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Best Local Similarity 74.6%; Pred. No. 2,7e-199;  
Matches 1242; Conservative 0; Mismatches 405; Indels 18; Gaps 5;

Qy 922 AACGAGAGTTCAAGGAGAGTGGTGGTCCAGTCCCATATTTACGAGAGTAGCA 981  
Db 1 AACGAGAGTTCAAGGAGAGTGGTGGTCCAGTCCCATATTTACGAGAGTAGCA 60  
Qy 982 GGAAGTCCCACTTCAGATGCAAAAGATATTAAGAAATCCAGATTCAAAAATC 1041  
Db 61 GGACAGTCCCACTTCAGATGCAAAAGATATTAAGAAATCCAGATTCGAGAAATC 120  
Qy 1042 CATGTGTTAGATTTAGACCAAAAGAAAGATGGTCTCAAGTCCACAGAGATGCAA 1101  
Db 121 CGTGTATTAGATTTAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180  
Qy 1102 CTTACGGCCATCTTAAGACACAGTGGAGAGCAAAAGCCCTCAAGTGAATCTCTG 1161  
Db 181 CTTATGGCCATCTTAAGAGGGCCATGACAGAGCAAAAGCCCTGATAGTCTACTG 240  
Qy 1162 TCTTTTGAATCCCAAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGAC 1221  
Db 241 TCTTTGATTTCCAAATTTGAAGTGAAGATCCATCATGGAGTCAAT...AGAGAC 297  
Qy 1222 AAGCAACCAAGATCTATCTCAGAGTACAGACTCAAAAGGCTGATTCAGCAAGCACTA 1281  
Db 298 AAACAACCAAGAACCTTACCTCAGAGTACAGACTCAAAAGGCTGATTCATCACTACTA 357  
Qy 1282 GAGNAGCAAAATCTTTGGATGTTGGGACAAATTCAGTTCATCATCAAAATTTGATCA 1341  
Db 358 GATGGAGACTGCTGCTTGGTGAAGGAAATTTCAATTCGTCGATGAGATTAAGTGGACA 417  
Qy 1342 CTGCGAGCTTTGGTCTGTACACCCCAATCAGAGTCCCAACATCTTTTGTGTTAAACA 1401  
Db 418 CT-----CTTCAGACTGTCACTGAACACAGACTGCCCCAAGCCCTTGTGATGTCA 471  
Qy 1402 GAGGATCTACTTTGAGTCCAGACTTCCTCTCTGTTGACCCAGCTTGGAGCAGTGGAC 1461  
Db 472 GAGGATCCCACTTTGAGTCCAGACTTCCTCTCTGTTGAGCCTTAGGCTTGGAGCAGTGGAC 531  
Qy 1462 GGAGCAGAGCATGGTCTPACCTGACATCTTTGTTGCTCCACCTGCTATGGCCCTTACCTCC 1521  
Db 532 AGAAGAGACTGAGCTGCTGACAGTTCTTGTCTCCACCTGATCAGCCTCAATTTCC 591  
Qy 1522 CTGTCAAGAGCTCAACCTTTCTTTATGGGATCAAGCATCTTCTCTGACTGATCAAGGC 1581  
Db 592 CGATCAGAAAATCTACCTTCGTTTA----CACCTAGCATCTTCTCTCTAGATGCTCAAGC 648

Qy 1582 ACCACAGATACAATGGCCACTGACACAGAAATGCTAGTACAGGGCTCACCATCCCCACC 1641  
Db 649 CCCCCCTCCCTGATGACCACTGGCCCAACAGCACTCATCCCCAAGCCCACTCTCCCACT 708  
Qy 1642 AGTGATTATCTGCAATCAGCAACTGCTCTGGAAATTTTCCATCCACCTGCACTCTCA 1701  
Db 709 ATGNTATTTTATACCATCCGCAATTTGCTTGAATGCTGATTTGGCTTGCATCTCTCC 768  
Qy 1702 GATGACAGCCGATCAAGTGGAGGAGATATGTCAGACACCTAGATGAATGAT 1761  
Db 769 AGTGACAGAGAGCTGATCACAAGCAGGCAATGACACAATCCGAGACCTAGATGGATGAT 828  
Qy 1762 CTGCTGACACTCTGCCCATCTGAGGTACCAAGCTCAGAGCTCAGGAATGTTCTGTCCA 1821  
Db 829 GTGCTGACAGCAGCCCTTGTGAGAAATATCAGAACTGAGTGGATAGATCTTGCCTCG 888  
Qy 1822 GATCATTTCTTGGAGGATACCACCTCTCTGCTCAGCTTTTACAGTATATCACCACCTAGTTCT 1881  
Db 889 GGTCAAGTTCTTGGAGATGACCAACCCATCCACAGTAGCGTTTCATCACCACAGCTCC 948  
Qy 1882 ATGACCATTTGCCCAAGGCGGAGAGCTGCTAGTGTCTTCACTGCTGCGTGTGCTAAC 1941  
Db 949 GAGACCAATTGCCCAAGGCGGAGAGCTAGTGTATTTCTTCAGCCTGCGTGTGCTAAC 1008  
Qy 1942 ATGGCTTTCTCCAAAGCACTTGTTCACAAGAGCTCTCTGGAGTACCGAGCTCTCGAGCAA 2001  
Db 1009 ATGGCTTTCTCTATGACCTTGTTCACAAGAGTCTCTGGAGTATCAAGCCCTGGAACAA 1068  
Qy 2002 CAATTCACAGCTGCTGTTCCATATCTAGATCCAAATCTTACAGGATTTAAGCACTT 2061  
Db 1069 CGATTTCAGACACTGCTGTTCCCTATCTAGATCGAATCTTACGGGATTTAAGCACTG 1128  
Qy 2062 GAAATCTTAACTTCAGAAACGGAGTGTGATCTGGAATAGCAAAATCAAGTTGCTTAAG 2121  
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Qy 2122 TCTGTGCGGTATACTCACAAGCTGTGCAAGGCTGTGCAAGGCTTTGGAGGATTTTCGTTGCT 2181  
Db 1189 CCGGTACCTTCAACCTCACCAGCGGTGCGCGGTCTTGGAGGATCTTCGGTCCACC 1248  
Qy 2182 GCAGCCCAACACTCCATCTGGAATAGACAGTACTCTCTCAACTTGAACAGCTGAT 2241  
Db 1249 CAGCTCAAGGGCTCAATCTGGAATCGAAAGTACTCCCTCGACATTTGAACAGCTGAT 1308  
Qy 2242 CAACGAGATCCCTGCAAGTTCTCGGCTGCGGGAATTTGCCAATGTGTAAAGAACGAA 2301  
Db 1309 CAGCGGATCCCTGCAAACTTCTAGACTGTGGCAAAATTTGCCAGTGTGTAAAGATGAG 1368  
Qy 2302 CGGACTGAGGAGCGGAGTGTGCTGCAAAACAGGATATGACAGCCAGGGAGCTGGAC 2361  
Db 1369 TGGACAGAGGAGCAGAGTGTGCTGACAGCAGGACATGAGAGCCACGGGACCTGGAC 1428  
Qy 2362 GGTCTGGAACACAGGCTCTGTGGCCCTGGCAAGAAATGCGAGTCTTCCAGGGAAG 2421  
Db 1429 TACCAGACCTTGAACCTCTGTCCCTTGG---AAGACTTGTGTGGCCGCGGAGAACAA 1485  
Qy 2422 GGAGCTCATGCGAGTGGCCAGATCACTCTGAAATCAAGCATCAAAAATAGTGTGTTAAA 2481  
Db 1486 CCAACTCCATCGAGGCAACAGATCACTTACAAACCAAGCTCAGGAACCTGTTGTTAAA 1545  
Qy 2482 AAGTTCCAAAATCAACAAATACAAAGTAAATCAGTAAAGAAATCTGAAATTAAGTAC 2541  
Db 1546 AAG---CTACGCTCAGCAAAATAGGTAGTGTAGTAAAGAAAGAAATCTTAACTATCAGCT 1602  
Qy 2542 GTAGAATATGAAGAAATTAACCATCAAGATTTGGGAAGGAATTA 2586  
Db 1603 ATAGATTTGAAGAAATTTGAAGACCAAGCTGAGGAGGAATTA 1647

RESULT 3  
AY415972  
LOCUS

AY415972 1587 bp DNA linear GSS 17-DEC-2003





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QY 2560 AACCATCAGATTGGGAAGGAATTA 2586
Db 1561 AACCATCAGATTGGGAAGGAATTA 1587

RESULT 4
LOCUS BGI96799 801 bp mRNA linear EST 21-APR-2001
DEFINITION R516026 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BGI96799
VERSION BGI96799.1 GI:13718486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 11329013
PUBMED
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 474.

FEATURES
source
1..801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 21.5%; Score 716.2; DB 12; Length 801;
Best Local Similarity 97.7%; Pred. No. 1.2e-148;
Matches 757; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

QY 2449 TCTGAAATCAAGCATCAAACTAGTGTGTTAAAGTTCCAAATCAACAAATCAACAG 2508
Db 23 TCTGAATATCAAGCATCAAACTAGTGTGTTAAAGTT-CAAATCAACAAATCAAG 81

QY 2509 GTAATCAGTAAAGAAATTCGAATCTAGTCCCTAGAGATATGAGAAATTAACCATCAA 2568
Db 82 GTAATCAGTAAAGAAATTCGAATCTAGTCCCTAGAGATATGAGAAATTAACCATCAA 141

QY 2569 GATTGGGAGGAATTAATAATGCAATATGACATATCTAGTCTATCTCAAGAGA 2628
Db 142 GATTGGGAGGAATTAATAATGCAATATGACATATCTAGTCTATCTCAAGAGA 201

QY 2629 GATGATTGGCTTCTCAAGGAAATGGAGACAGGCATATTCATGGGTCAATCAAAATCCAG 2688
Db 202 GATGATTGGCTTCTCAAGGAAATGGAGACAGGCATATTCATGGGTCAATCAAAATCCAG 261

QY 2689 ACATACAGTCAACACTGAGATCAGCACACACCATATTTCAATATAGAGACTCATGA 2748
Db 262 ACATACAGTCAACACTGAGATCAGCACACACCATATTTCAATATAGAGACTCATGA 321

2749 CTTGGCAACCAAGTAATTTCTGAAAGAAAGACACTTACTTATTTATTAAGCCCAATGC 2809
322 CTTGGCAACCAAGTAATTTCTGAAAGAAAGACACTTACTTATTTATTAAGCCCAATGC 381
2809 AATCAGCGAAACATATTTTACTTCTTGGATGATAGTCAAAATGATCATAAAGCCAGGT 2868
382 AATCAGCGAAACATATTTTACTTCTTGGATGATAGTCAAAATGATCATAAAGCCAGGT 441
2869 TTGCTTCACCTTCCCTGAAATTTTACTTACAGATCAATTTGCAACAGCATAGCTTACT 2928
442 TTGCTTCACCTTCCCTGAAATTTTACTTACAGATCAATTTGCAACAGCATAGCTTACT 501
2929 TATCTTTAGGAGCTGAACAATTTATTTGGGAAGCAAACTCTTTATATGCTAGAAAGTACA 2988
502 TATCTTTAGGAGCTGAACAATTTATTTGGGAAGCAAACTCTTTATATGCTAGAAAGTACA 561
2989 TTTAAAAAGATGACTACTTACGACGAGAGATGAGGTCTCTCTAAACGATGAATGTATGT 3048
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3049 AGTGTGTAGGCACTAGTGTATATATGCTCCACACTACGCTCTGATAAACACAAAC 3108
622 AGTGTGTAGGCACTAGTGTATATATGCTCCACACTACGCTCTGATAAACACAAAC 681
3109 CTCAGTATTCAGTTATTAGGCACACTAGTTTATATGCAACTACTGCTTACATAGTAGAC 3168
682 CTCAGTATTCAGTTATTAGGCACACTAGTTTATATGCAACTACTGCTTACATAGTAGAC 741
3169 TGTTTTGTGCAATTAATCTTTGAATTTCTTTAAAGAACTGAGGTTAGAT 3223
742 TGTTTTGTGCAATTAATCTTTGAATTTCTTTAAAGAACTGAGGTTAGAT 794

RESULT 5
LOCUS B1752112
DEFINITION B1752112 836 bp mRNA linear EST 25-SEP-2001
ACCESSION B1752112
VERSION B1752112.1 GI:15743690
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11482 row: 1 column: 16
High quality sequence stop: 822.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5192991"
/lab_host="DH10B"
/clone_lib="NIH MGC 114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
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range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

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ORIGIN
Query Match      19.2%; Score 640.2; DB 12; Length 836;
Best Local Similarity 96.8%; Pred. No. 1e-131;
Matches 693; Conservative 0; Mismatches 18; Indels 5; Gaps 4;
QY 2232 ACCAGCTGATCAAGCAGATCCCTCCAGATTTCTCGCTGGCGGCAATTTGCCCAATGTGT 2291
DB 122 AACACCTGATCAAGCAGATCCCTCCAGATTTCTCGCTGGCGGCAATTTGCCCAATGTGT 181
QY 2292 AAAGAACGACGAGCTGAGGAAGCGGAGTGTGCTGCAAAACGAGATATGACAGCCAGGG 2351
DB 182 AAAGAACGACGAGCTGAGGAAGCGGAGTGTGCTGCAAAACGAGATATGACAGCCAGGG 241
QY 2352 GAGCTGGACGGTCTGGAAACGAGCCCTCTGTGGCCCTGGCAAGGAATGCCAGGTCT 2411
DB 242 GAGCTGGACGGTCTGGAAACGAGCCCTCTGTGGCCCTGGCAAGGAATGCCAGGTCTCT 301
QY 2412 CCAGGAAAGGAGCTCCATCAGAGTTGCCAGATCATCTTGAAATCAAGCATCAAAAC 2471
DB 302 CCAGGAAAGGAGCTCCATCAGAGTTGCCAGATCACTCTGAAATCAAGCATCAAAAC 361
QY 2472 TAGTGTAAAAGTTCCAAATCAACAAATCAACAGGTATCACTGAAAAGAAATCTGA 2531
DB 362 TAGTGTAAAAGTTCCAAATCAACAAATCAACAGGTATCACTGAAAAGAAATCTGA 421
QY 2532 ATTACTGACCGTAGAATATGAAGAAATTTAACCATCAAGATGGGAAGAAATTAAGAACT 2591
DB 422 ATTACTGACCGTAGAATATGAAGAAATTTAACCATCAAGATGGGAAGAAATTAAGAACT 481
QY 2592 GAAATGTACAAATATCATCTTAGCTATCTCAAGAGAGATGTTGCTCTTCAAGGAAA 2651
DB 482 GAAATGTACAAATATCATCTTAGCTATCTCAAGAGAGATGTTGCTCTTCAAGGAAA 541
QY 2652 ATGAGACAGGCATATTCATGGGTCAACAAATCCAGACATACAGTCAACACACTGAGAATC 2711
DB 542 ATGAGACAGGCATATTCATGGGTCAACAAATCCAGACATACAGTCAACACACTGAGAATC 601
QY 2712 AGCACAACCATATTTCAATATAGAGAGTCATGCTTGGCAACAGATAATCTGAA 2771
DB 602 AGCACAACCATATTTCAATATAGAGAGTCATGCTTGGCAACAGATAATCTGAA 661
QY 2772 -AAAAAGACACTTACTTATTTATTAACCCCAATGCAATCAGCAGAAACATATTTTAC 2830
DB 662 GAAACAGACACTTACTTATTTATTT--ACCAAAATGCAATCAGCGGAAACATATTTTAC 719
QY 2831 TATTCTTGGATGATAGTCAAAA--TGATCATAGCCAGGTTTGTTCACCTTCCCTGAAA 2889
DB 720 TATTCTTGGATGATAGTCAAAAATGATCATAGCCAGGTTTGTTCACCTTCCCTGAAA 779
QY 2890 ATTTTACTCAGACATCTTCCACACAGCATTA-GCTTACTTATTTGTTTGGGACTG 2944
DB 780 ATTTTACTCAGACATCTTCCACACAGCATAGGCTTACTTATTTGTTAAGGACTG 835
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RESULT 6
BX510244
LOCUS DXFzp686P2496_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DXFzp686P2496 5', mRNA sequence.
ACCESSION BX510244
VERSION BX510244.1 GI:32050551
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 690)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
```

Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.  
EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., et al.)  
Unpublished (2003)  
Contact: MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686P2496) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
1..690  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="DKFZp686P2496"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiI; cDNA-collection"

#### FEATURES

source

#### ORIGIN

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Query Match      19.0%; Score 634; DB 13; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.4e-130;
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAACCAAGAGGTTATCTCAATCATCTGTCATCATATATATATATATTTTTCACATTTC 60
DB 57 TAAACCAAGAGGTTATCTCAATCATCTGTCATCATATATATATATATTTTTCACATTTC 116
QY 61 TGTACTTTTTTAATGAGATTTGAGGTTTCTGTGTAATTTATCAGAAATACCAATGCAC 120
DB 117 TGTACTTTTTTAATGAGATTTGAGGTTTCTGTGTAATTTATCAGAAATACCAATGCAC 176
QY 121 AAAAGCCAGATGTATTTGGAACTAGAGAGCTATTTTGTGTTTTCGATTTCCTCA 180
DB 177 AAAAGCCAGATGTATTTGGAACTAGAGAGCTATTTTGTGTTTTCGATTTCCTCA 236
QY 181 AGTTCAGGAACCAAGATATCTCCATTAACATATACCATTCTGAAACTAAAGACATAGA 240
DB 237 AGTTCAGGAACCAAGATATCTCCATTAACATATACCATTCTGAAACTAAAGACATAGA 296
QY 241 CAATCCCCCAAGATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTAT 300
DB 297 CAATCCCCCAAGATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTAT 356
QY 301 GAGAGCATATTCGATTTGGCAAGCATCGAACAAAAAGATCCGATTTTCCCAACGGG 360
DB 357 GAGAGCATATTCGATTTGGCAAGCATCGAACAAAAAGATCCGATTTTCCCAACGGG 416
QY 361 GGTAAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGACAGCTTCTCAAGCTTATTA 420
DB 417 GGTAAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGACAGCTTCTCAAGCTTATTA 476
QY 421 TAGATTGAGAGTGTCTCAGGAGCAGTATGGAGCATATCGGATCTTCTTGGATCGCAT 480
DB 477 TAGATTGAGAGTGTCTCAGGAGCAGTATGGAGCATATCGGATCTTCTTGGATCGCAT 536
QY 481 CCTGACACAGGGGAATATCAGGACTGGGTTCAGCATCTGCCAGCAGGAGACTTCTTGCT 540
DB 537 CCTGACACAGGGGAATATCAGGACTGGGTTCAGCATCTGCCAGCAGGAGACTTCTTGCT 596
QY 541 CTTTGCATTTGAAAAAATCTTCAGCAATCCAGAGGACCTGGATCTTCTCCACAGAG 600
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Db 597 CTTTGACATTGGRAAACTTCAGCAATTCAGGAGCACCCTGATCTCTCCAGCAGAG 656
601 AATPAAACAGAGAGTTTCCTGACAGAAAGAT 634
Db 657 AATPAAACAGAGAGTTTCCTGACAGAAAGAT 690

RESULT 7
BM695987 633 bp mRNA linear EST 28-FEB-2002
UI-E-CL1-afa-m-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
UI-E-CL1-afa-m-11-0-UI 5', mRNA sequence.
BM695987
VERSION BM695987.1 GI:19009245
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Ronaldo M.F., Lennon G. and Soares M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CL1-afa-m-11-0-UI"
/tissue_type="human retina"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CL1"
/note="Organ: eye; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CL1 is a normalized cDNA library containing the
following tissue(s): retina. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCGCG. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
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## ORIGIN

```

Query Match 18.9%; Score 628.8; DB 12; Length 633;
Best Local Similarity 99.5%; Pred. No. 3 5e-129;
Matches 630; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2529 TGAATTACTGACCGTAGAATATGAGAAATTTACCATCAAGATTGGGAGGAAATTAATA 2588
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Db 1 TGAATTACTGACCGTAGAATATGAGAAATTTACCATCAAGATTGGGAGGAAATTAATA 60
2589 ACTGAAAATGTACAAATTTATCACTTAGCTATCTCAAGAGAGATGATTTGCTTCTCAAGG 2648
Db 61 ACTGAAAATGTACAAATTTATCACTTAGCTATCTCAAGAGAGATGATTTGCTTCTCAAGG 120
2649 AAAATGGAGACAGGCATATTCATGGGGTCATCAAAATCCAGACATACAGTCAACACTCAGA 2708
Db 121 AAAATGGAGACAGGCATATTCATGGGGTCATCAAAATCCAGACATACAGTCAACACTCAGA 180
2709 ATCAGCACACACCATATTTTCAAAATATAGAAGTCACTTGGCAACACAGTAAATTTCT 2768
Db 181 ATCAGCACACACCATATTTTCAAAATATAGAAGTCACTTGGCAACACAGTAAATTTCT 240
2769 GAAAAAAGACACTTACTTATTATTAACCCCAATGCAATCAGCGAAACATATTTTT 2828
Db 241 GAAAAAAGACACTTACTTATTATTAACCCCAATGCAATCAGCGAAACATATTTTT 300
2829 ACTATTCTTGGATGATAGTCAAAATGATCAATAAGCCAGGTTTGGCTTCCACCTTCCCTGAA 2888
Db 301 ACTATTCTTGGATGATAGTCAAAATGATCAATAAGCCAGGTTTGGCTTCCACCTTCCCTGAA 360
2889 AATTTTACTCAGATCATTTTGCAACAGCATAGCTTACTTATTTAGGAGCTGAACA 2948
Db 361 AATTTTACTCAGATCATTTTGCAACAGCATAGCTTACTTATTTAGGAGCTGAACA 420
2949 ATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTAC 3008
Db 421 ATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTAC 480
3009 GCAGGAGATGCGAGGCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATGATG 3068
Db 481 GCAGGAGATGCGAGGCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATGATG 540
3069 AGTGTATATATGCTCCACACTAGTCTGTATAACACACAAACCTCAGTATTCAGTTATTAGG 3128
Db 541 AGTGTATATATGCTCCACACTAGTCTGTATAACACACAAACCTCAGTATTCAGTTATTAGG 600
3129 CACACTAGTTTATAGCGAACTACTGCTTACAT 3161
Db 601 CACACTAGTTTATAGCGAACTACTGCTTACAT 633

RESULT 8
BM695987 626 bp mRNA linear EST 15-JUL-2002
LOCUS hd33d04.v1 Human Retina cDNA (Un-normalized, unamplified): hd/ne
DEFINITION Homo sapiens cDNA clone hd33d04 5', mRNA sequence.
ACCESSION BM695987
VERSION BM695987.1 GI:21763724
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS Wistow G., Bernstein S.L., Wyatt M.K., Ray S., Behal A.,
Touchman J.W., Bouffard G., Smith D. and Peterson K.
TITLE Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE 2103461
PUBMED 12107411
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 495 0078
Email: Graeme@helix.nih.gov
Plate: 33 row: d column: 04
Seq primer: M13RP1 reverse primer (ABI).
```

FEATURES  
source

Location/Qualifiers  
1. .626  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="hd33d04"  
/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
BioServe Biotechnology (Laurel MD) essentially following  
the protocols of the SuperScript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (<http://www.lifetech.com/>). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTCTAGATCGGAGCGGCCG(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 18.8%; Score 626; DB 13; Length 626;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 968 ACCAGGAGCTAGCAGGAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAG 1027  
DB 1 ACCAGGAGCTAGCAGGAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAG 60

QY 1028 GATTCAAAAATCATGTGTAGATTAGACCAAGAGAAAGATGGCTCAAGCT 1087  
DB 61 GATTCAAAAATCATGTGTAGATTAGACCAAGAGAAAGATGGCTCAAGCT 120

QY 1088 CCACAGAGATCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAAGCCCTG 1147  
DB 121 CCACAGAGATCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAAGCCCTG 180

QY 1148 CAAGTGACCTCTGTTGATTCGCAAAATGAAAGTGAAGAGTCTATCATGGAA 1207  
DB 181 CAAGTGACCTCTGTTGATTCGCAAAATGAAAGTGAAGAGTCTATCATGGAA 240

QY 1208 CCATGGAGGAGCAGCAACCAAGATCTATCTCAGAGCTACAGACTCAAAAGGCTGA 1267  
DB 241 CCATGGAGGAGCAGCAACCAAGATCTATCTCAGAGCTACAGACTCAAAAGGCTGA 300

QY 1268 TCAGCAAGACCTAGAGGAAGCAATCTTTGGATGTGGGACAAATTCAGTTCACGTATG 1327  
DB 301 TCAGCAAGACCTAGAGGAAGCAATCTTTGGATGTGGGACAAATTCAGTTCACGTATG 360

QY 1328 AAATGCTGGATCACTGCCAGCTTTGGTCTGACCCATCAGAGCTGCCACATCTT 1387  
DB 361 AAATGCTGGATCACTGCCAGCTTTGGTCTGACCCATCAGAGCTGCCACATCTT 420

QY 1388 TTGCTGTTTATAACAGAGATGCTACTTTAGTTCAGAACTTCTCTCTGTTGAACCCGAGC 1447  
DB 421 TTGCTGTTTATAACAGAGATGCTACTTTAGTTCAGAACTTCTCTCTGTTGAACCCGAGC 480

QY 1448 TTGACAGAGTGGAGCAGAGATGGTCTACCTGACACTTCTTGCTCTCCACCTGCTA 1507  
DB 481 TTGACAGAGTGGAGCAGAGATGGTCTACCTGACACTTCTTGCTCTCCACCTGCTA 540

QY 1508 TGGCTCTTACCTCCCTGTGCAAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTC 1567  
DB 541 TGGCTCTTACCTCCCTGTGCAAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTC 600

QY 1568 TGACTGATCAAGGCAACCCAGATACA 1593

DB

601 TGACTGATCAAGGCACCCACAGATACA 626

RESULT 9

BQ638902

LOCUS

DEFINITION BQ638902 622 bp mRNA linear EST 15-JUL-2002  
hd29a06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he

ACCESSION

BQ638902

VERSION

BQ638902.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 622)

AUTHORS

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,

TITLE

Expressed sequence tag analysis of human retina for the NEIBank

JOURNAL

Mol. Vis. 8 (4), 196-204 (2002)

MEDLINE

22103461

PUBMED

12107411

COMMENT

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 29 row: a column: 06

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1. .622

FEATURES

source

/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="hd29a06"  
/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
BioServe Biotechnology (Laurel MD) essentially following  
the protocols of the SuperScript plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (<http://www.lifetech.com/>). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTCTAGATCGGAGCGGCCG(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 18.5%; Score 617.2; DB 13; Length 622;  
Best Local Similarity 99.5%; Pred. No. 1.3e-126;  
Matches 619; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2480 AAAGTTCCTCAAAATCAACAAATACAGGTAATCAGTAAAGAAATCTCAATCTACTGA 2539  
DB 1 AAAGTTCCTCAAAATCAACAAATACAGGTAATCAGTAAAGAAATCTCAATCTACTGA 60

QY 2540 CGGTAGAATATGAAGAAATTTAACCATCAAGATGGGAGGAAATTAATAAATCTGAAATGT 2599  
DB 61 CGGTAGAATATGAAGAAATTTAACCATCAAGATGGGAGGAAATTAATAAATCTGAAATGT 120

QY 2600 ACAATATCACTTAGCTATCTCAAGAGAGATGATTTCCCTTCTCAAGGAAATGAGAC 2659

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Db 121 ACAATATCAATTAGGCTATCTCAGAGAGATGATTTGCTTCTCAGGAAATGGAGAC 180
QY 2660 AGGCATATTCATGGTGTATCAAAATCCAGATACAGTCAACACTGAGATCAGACACA 2719
Db 181 AGGCATATTCATGGTGTATCAAAATCCAGATACAGTCAACACTGAGATCAGACACA 240
QY 2720 CCATATTTCAATATAGAGAGTCTATGTTGGCAACAGTAAATCTGAAAAAAGA 2779
Db 241 CCATATTTCAATATAGAGAGTCTATGTTGGCAACAGTAAATCTGAAAAAAGA 300
QY 2780 CACTTACTTATTTAAACCCCAATCAATCAGCGAAACATATTTTACTATCTTGG 2839
Db 301 CACTTACTTATTTAAACCCCAATCAATCAGCGAAACATATTTTACTATCTTGG 360
QY 2840 ATGATAGTCAAAATGATCATAGCCAGGTTTGGCTCCACCTTCCCTGAAATTTTACTCA 2899
Db 361 ATGATAGTCAAAATGATCATAGCCAGGTTTGGCTCCACCTTCCCTGAAATTTTACTCA 420
QY 2900 CAGATCAATTTGCAACAGCATAGTCTTACTTATTTAGGACCTGCAACATTTATTTGGGA 2959
Db 421 CAGATCAATTTGCAACAGCATAGTCTTACTTATTTAGGACCTGCAACATTTATTTGGGA 480
QY 2960 AGCAAACTCTTTATATGATAGAGTACATTTAAAGATGACTTACTTACGAGGAGATG 3019
Db 481 AGCAAACTCTTTATATGATAGAGTACATTTAAAGATGACTTACTTACGAGGAGATG 540
QY 3020 CAGGTCCTCTAAACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3079
Db 541 CAGGTCCTCTAAACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 3080 GCTCCACACTAGCTCTGATAAA 3101
Db 601 GCTCCACACTAGCTCTGATAAA 622

RESULT 10
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LOCUS UI-E-CKO-aas-h-07-0-UI.r1 UI-E-CKO Homo sapiens cDNA clone
DEFINITION UI-E-CKO-aas-h-07-0-UI 5', mRNA sequence.
ACCESSION BM685921
VERSION BM685921.1 GI:18995817
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITILE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
1..653
/organism="Homo sapiens"
/mol_type="mRNA"
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/db xref="taxon:9606"
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/dev_stages="adult"
/lab_host="DH103 (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CKO"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CKO is a cDNA library containing the following
tissue(s): Retina Foveal and Macular. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is GFFC.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
(NEI)."
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## ORIGIN

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Query Match 18.5%; Score 615.6; DB 12; Length 653;
Best Local Similarity 99.4%; Pred. No. 3.1e-126;
Matches 618; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2709 ATCAGCACACACATATTTCAATATAGAGAGTCACTGCTTGGCAACCACTAAATCT 2768
Db 10 AACAGCACACACATATTTCAATATAGAGAGTCACTGCTTGGCAACCACTAAATCT 69
QY 2769 GAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTT 2828
Db 70 GAAGAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTT 129
QY 2829 ACTATTTCTGGATAGTCAAAATGATCAAGCCAGGTTTGCCTCCACCTTCCCTGAA 2888
Db 130 ACTATTTCTGGATAGTCAAAATGATCAAGCCAGGTTTGCCTCCACCTTCCCTGAA 189
QY 2889 AATTTTACTCACAGATCATTTTGCACCAAGCATAGCTTACTTATTTGTTAGGCACTGAACA 2948
Db 190 AATTTTACTCACAGATCATTTTGCACCAAGCATAGCTTACTTATTTGTTAGGCACTGAACA 249
QY 2949 ATTATTTGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTAC 3008
Db 250 ATTATTTGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTAC 309
QY 3009 GCAGGAGATGCAAGTCTCTCTAAACGATGAATGATGATGATGATGATGATGATGATG 3068
Db 310 GCAGGAGATGCAAGTCTCTCTAAACGATGAATGATGATGATGATGATGATGATGATG 369
QY 3069 AGTGTATATATGCTCCACACTACGCTCTGATAAACAACCAACCTCAGTATTCAGTTATTAGG 3128
Db 370 AGTGTATATATGCTCCACACTACGCTCTGATAAACAACCAACCTCAGTATTCAGTTATTAGG 429
QY 3129 CACACTAGTTTTTATACGCAACTACTGCTTACATAGTACTGTTTGTGTTGTTGTTGTTGTTGTT 3188
Db 430 CACACTAGTTTTTATACGCAACTACTGCTTACATAGTACTGTTTGTGTTGTTGTTGTTGTTGTT 489
QY 3189 TTGAATTTGTTCTTTTAAAGAAACTGAGGTTTCAGATACACATACCATGGAATAATCTTACT 3248
Db 490 TTGAATTTGTTCTTTTAAAGAAACTGAGGTTTCAGATACACATACCATGGAATAATCTTACT 549
QY 3249 TTCTTTGTTTACTACCAAGCTATTTTAAAGAGATGCTATGTTGTTGTTGTTGTTGTTGTTGTTGTT 3308
Db 550 TTCTTTGTTTACTACCAAGCTATTTTAAAGAGATGCTATGTTGTTGTTGTTGTTGTTGTTGTTGTT 609
QY 3309 TGTACTATATGACATAATCAAT 3330
Db 610 TGTACTATATGACATAATCAAT 631
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RESULT 11
BM690735
LOCUS
DEFINITION
  UI-B-CK0-aav-c-12-0-UI.r1 UI-B-CK0 Homo sapiens cDNA clone
  UI-B-CK0-aav-c-12-0-UI 5', mRNA sequence.
ACCESSION
  BM690735
VERSION
  BM690735.1 GI:19003993
KEYWORDS
  EST.
SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 675)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
JOURNAL
  97044477
MEDLINE
  8889548
PUBMED
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
FEATURES
    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="UI-B-CK0-aav-c-12-0-UI"
        /tissue_type="Retina Foveal and Macular"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
        /clone_lib="UI-B-CK0"
        /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
        modified polylinker; Site 1: EcoR I; Site 2: Not I;
        UI-B-CK0 is a cDNA library containing the following
        tissue(s): Retina Foveal and Macular. The library was
        constructed according to Bonaldo, Lennon and Soares,
        Genome Research, 6:791-806, 1996. First strand cDNA
        synthesis was primed with an oligo-dT primer containing a
        Not I site. Double stranded cDNA was ligated to an EcoR I
        adaptor, digested with Not I, and cloned directionally
        into pT7T3-Pac vector. The oligonucleotide used to prime
        the synthesis of first-strand cDNA contains a library tag
        sequence that is located between the Not I site and the
        (d)T18 tail. The sequence tag for this library is GTCC.
        This library was created for the program, Gene Discovery
        in the Visual System, supported by National Eye Institute
        (NEI)."
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## ORIGIN

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Query Match      17.7%; Score 589.4; DB 12; Length 675;
Best Local Similarity 99.7%; Pred. No. 2.1e-120;
Matches 601; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2728 CAAATATAGACAGTCATGCTACTTGGCAACAGTAAATCTGAAAAAAGACACTTACT 2787
Db 8 CAAATATAGAGA-TCATGTACTTGGCAACAGTAAATCTGAAAAAAGACACTTACT 66

QY 2788 TATTATTAAACCCCAATGCAATCAGCGAAACATATTTTACTATTCTTGATGATAGT 2847
Db 67 TATTATTAAACCCCAATGCAATCAGCGAAACATATTTTACTATTCTTGATGATAGT 126
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QY 2848 CAAATATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTACTACAGATCAT 2907
Db 127 CAAATATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTACTACAGATCAT 186
QY 2908 TTGCACACAGCATAGCTTACTTATTGTTTGGGACTGAACTATTTATTGGGAAGCAAACT 2967
Db 187 TTGCACACAGCATAGCTTACTTATTGTTTGGGACTGAACTATTTATTGGGAAGCAAACT 246
QY 2968 CTTTATATGCTAGAAAGTACATTTAAAGATGACTTACGCGAGGAGATGCGAGTCTC 3027
Db 247 CTTTATATGCTAGAAAGTACATTTAAAGATGACTTACGCGAGGAGATGCGAGTCTC 306
QY 3028 TCTTAACGCGATCAATGCTATGTTAGTGTAGGACACGTAGTGTATATATGCTCCACA 3087
Db 307 TCTTAACGCGATCAATGCTATGTTAGTGTAGGACACGTAGTGTATATATGCTCCACA 366
QY 3088 CTACGTCTGATAAACAACAACCTCAGTATTTCAGTTATTAGGCACACTAGTTTATACGCA 3147
Db 367 CTACGTCTGATAAACAACAACCTCAGTATTTCAGTTATTAGGCACACTAGTTTATACGCA 426
QY 3148 ACTACTGCTTACATAGTACTGTTTGTGTCATATATCTTTGAATGTTCTTTTAAAAG 3207
Db 427 ACTACTGCTTACATAGTACTGTTTGTGTCATATATCTTTGAATGTTCTTTTAAAAG 486
QY 3208 AACTGAGGTTTCAGATACACATACCATGAAAAATCTTACTTTCTTGTACTACACAAA 3267
Db 487 AACTGAGGTTTCAGATACACATACCATGAAAAATCTTACTTTCTTGTACTACACAAA 546
QY 3268 GCTATTTTAAAGAAAGTCTATGTTGGGGAAGGCGAAGTTGTACTATATGACATATC 3327
Db 547 GCTATTTTAAAGAAAGTCTATGTTGGGGAAGGCGAAGTTGTACTATATGACATATC 606
QY 3328 AAT 3330
Db 607 AAT 609

RESULT 12
BQ636596
LOCUS
DEFINITION
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  Homo sapiens cDNA clone hd11h02 5', mRNA sequence.
ACCESSION
  BQ636596
VERSION
  BQ636596.1 GI:21761055
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 598)
  Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
  Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
  Expressed sequence tag analysis of human retina for the NEIRank
  Project: Retbindin, an abundant, novel retinal cDNA and alternative
  splicing of other retina-preferred gene transcripts
  Mol. Vis. 8 (4), 196-204 (2002)
JOURNAL
  22103461
MEDLINE
  12107411
PUBMED
  Contact: Wistow G
  Section on Molecular Structure and Function
  National Eye Institute
  6/331, NIH, Bethesda, MD 20892-2740, USA
  Tel: 301 402 3452
  Fax: 301 496 0078
  Email: graeme@helix.nih.gov
  Plate: 11 row: h column: 02
  Seq primer: M13RPI reverse primer (ABI).
FEATURES
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="hd11h02"
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/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/notes="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pACAGTCTAGATCGGAGCGGCGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
```

ORIGIN

Query Match 17.3%; Score 577.6; DB 13; Length 598;  
Best Local Similarity 99.3%; Pred. No. 8.9e-118;  
Matches 580; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1490 CTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCTCCACCTTTCTTTATGG 1549  
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Db 15 CTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCTCCACCTTTCTTTATGG 74  
| | | | |  
QY 1550 CATCAAGCATCTTCTCTCTGATCTGATCAAGGACCAACAGATCAATGGCCATGACCGA 1609  
| | | | |  
Db 75 CATCAAGCATCTTCTCTCTGATCTGATCAAGGACCAACAGATCAATGGCCATGACCGA 134  
| | | | |  
QY 1610 CAATGCTAGTACAGGCGCTCACCATCCACAGTGAATTTCTGCAATCAGCCAACTGG 1669  
| | | | |  
Db 135 CAATGCTAGTACAGGCGCGACCATCCACAGTGAATTTCTGCAATCAGCCAACTGG 194  
| | | | |  
QY 1670 CTCCTGGAAATTTCCATCCACCTGCTCTTCAGATGACAGCGCATCAAGTGCAGTGGCG 1729  
| | | | |  
Db 195 CTCCTGGAAATTTCCATCCACCTGCTCTTCAGATGACAGCGCATCAAGTGCAGTGGCG 254  
| | | | |  
QY 1730 AGATATGCTGACACACCTAGATGAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1789  
| | | | |  
Db 255 AGATATGCTGACAGACCTAGATGAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 314  
| | | | |  
QY 1790 TACAGAGCTCAGCGAATATGTTTCTGTCGCCAGATCATTTCTTGGAGGATACCATCTCTG 1849  
| | | | |  
Db 315 TACAGAGCTCAGCGAATATGTTTCTGTCGCCAGATCATTTCTTGGAGGATACCATCTCTG 374  
| | | | |  
QY 1850 TCTCAGCTTTACAGTATATACCACTAGTCTTATGACCAATTCGCCCAAGGCGCGAGAGC 1909  
| | | | |  
Db 375 TCTCAGCTTTACAGTATATACCACTAGTCTTATGACCAATTCGCCCAAGGCGCGAGAGC 434  
| | | | |  
QY 1910 TGGTAGTGTCTTTCAGTCTGCGTGTGCTAAAGATGCGCTTCTCCAAAGCAGCTGTTCAACA 1969  
| | | | |  
Db 435 TGGTAGTGTCTTTCAGTCTGCGTGTGCTAAAGATGCGCTTCTCCAAAGCAGCTGTTCAACA 494  
| | | | |  
QY 1970 AGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAAATTCACAGCTGTGGTTCATATC 2029  
| | | | |  
Db 495 AGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAAATTCACAGCTGTGGTTCATATC 554  
| | | | |  
QY 2030 TAGATCCCAATCTTACAGATTTTAAAGCACTTGAATCTTAAC 2073  
| | | | |  
Db 555 TAGATCCCAATCTTACAGATTTTAAAGCACTTGAATCTTAAC 598  
| | | | |

RESULT 13  
CA393958  
LOCUS  
DEFINITION  
584904.y1 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs44904  
5', mRNA sequence.  
CA393958  
ACCESSION

CA393958.1 GI:24728064  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 508)  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
TITLE Expressed sequence tag analysis of human RPE/choroid for the  
NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
MEDLINE 22103460  
PUBMED 12107410  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 44 row: 9 column: 04  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1. 508  
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/clone="cs44904"  
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/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp.  
<http://www.invitrogen.com/>). The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 15.0%; Score 498.4; DB 14; Length 508;  
Best Local Similarity 98.8%; Pred. No. 3.9e-100;  
Matches 502; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1442 CCCAGCTTGAGACAGTGGACGGACGAGCATGCTTACCTGACACTTCTTGGTCTCCAC 1501  
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Db 1 CCCAGCTTGAGACAGTGGACGGACGAGCATGCTTACCTGACACTTCTTGGTCTCCAC 60  
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QY 1502 CTGCTATGGCTCTACCTCCCTGTGAGAAGCTCCACTTTCTTTATGGCATCAAGCATCT 1561  
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Db 241 CACATCCACTGTGATCTTTCAGATGACAGCCGATCAAGTGCAGTGGCAGAGATATGTC 300  
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QY 1742 GACACCTAGATGAATGGATCTGTCTGACACTCTCTGCCCATCTGAGGTACAGAGCTCA 1801
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RESULT 14
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LOCUS BX097138 Soares retina N2b4HR Homo sapiens cDNA clone
DEFINITION IMAG998N11359 ; IMAGE:190666, mRNA sequence.
ACCESSION BX097138
VERSION BX097138.1 GI:27843098
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 472)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAG998N11359.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/cloncards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGGAACACAGCTATGAC.
FEATURES
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/notes="Organ: eye; Vector: pRT73D (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the

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University of Toronto. Library constructed by Bento  
Soares and M.Fatima Bonaldo. "

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ORIGIN
Query Match 14.2%; Score 472; DB 13; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.9e-94;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1  GGACAAATTCAGTTCACTGATGAATTTGCTGCTTAAACAGAGGATGCTTACTTTGAGTCCAGAAC 1366
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QY 1367 AATCAGAGCTGCCACATCTTTGCTGCTTAAACAGAGGATGCTTACTTTGAGTCCAGAAC 1426
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Db 61  AATCAGAGCTGCCACATCTTTGCTGCTTAAACAGAGGATGCTTACTTTGAGTCCAGAAC 120
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Db 421  GCGAAGATATGTCAGACACCTAGATGAATGGATCTGTCTGACACTCTCTGC 472
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RESULT 15
W26960/c 561 bp mRNA linear EST 08-MAY-1996
LOCUS W26960 Human retina cDNA randomly primed sublibrary Homo sapiens
DEFINITION cDNA, mRNA sequence.
ACCESSION W26960
VERSION W26960.1 GI:1306188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS Macke, J., Smallwood, P. and Nathans, J.
TITLE Adult Human Retina cDNA
JOURNAL Unpublished (1996)
COMMENT Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy.nathans@gmail.bs.jhu.edu
Clones from this library are NOT available.
PCR Primers
FORWARD: CTTTGTGCAAGTTCAGCTGTTAAGT
BACKWARD: GAGTGGCTTATGATATTTCTTCCAGGGTAA
Seq primer: GGGTAAAGCAAAAGAAATT.
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Site 2: EcoRI; The library used for sequencing was a  
sublibrary derived from a human retina cDNA library.  
Inserts from retina cDNA library DNA were isolated,  
randomly primed, PCR amplified, size-selected, and cloned  
into lambda gt10. Individual plaques were arrayed and  
used as templates for PCR amplification, and these PCR  
products were used for sequencing."
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ORIGIN

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Query Match      13.8%; Score 459.6; DB 14; Length 561;  
Best Local Similarity 93.4%; Pred. NO. 1.7e-91;  
Matches 493; Conservative 0; Mismatches 33; Indels 2; Gaps 2;  
  
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QY 1283 AGGAGAGACAATCTTTGGATGTGGGACAAATTCAGTTCAGTCACTGATGAAATTTGCTGATCAC 1342  
Db      |||||  
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413  TGCCAGCCTTTGGTCTGTGACACCAATCAGAGCTGCCACATCTTTTGTGTTATAACAG 354  
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QY 1463 GAGCAGAGCATGGTCTTACTGACACTTTTGTCTCTCCACCTGCTATGSCCTTACCTCCC 1522  
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Search completed: March 1, 2004, 20:29:00  
Job time : 8160 secs



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; Sequence 27, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 3261  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 isoform A variant cDNA sequence  
; NAME/KEY: CDS  
; LOCATION: (128)..(2440)  
US-10-007-270-27  
  
Query Match 93.8%; Score 3124.6; DB 13; Length 3261;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 3256; Conservative 0; Mismatches 5; Indels 69; Gaps 6;  
  
Qy 1 TAAACCAAGAGGTTATCTCTCAATCATCTGTCATCAATATATATATATATATATATATAT 60  
Db 1 TAAACCAAGAGGTTATCTCTCAATCATCTGTCATCAATATATATATATATATATATATAT 58  
  
Qy 61 TGTACTTTTTTAATGAGATTGAGGTTGTCGTGATGATGATGATGATGATGATGATGATGAT 120  
Db 59 TGTACTTTTTTAATGAGATTGAGGTTGTCGTGATGATGATGATGATGATGATGATGATGAT 117  
  
Qy 121 AAAAGCCAGAGATGATTTGGAACTAGAGAGCTATTTTGTGTTTGTGTTTGTGTTTGTGTTT 180  
Db 118 AAAAGCCAGAGATGATTTGGAACTAGAGAGCTATTTTGTGTTTGTGTTTGTGTTTGTGTTT 177  
  
Qy 181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACATTCGAACTAAGACATAGA 240  
Db 178 AGTTCAAGGAACCAAGATATCTCCATTAACATATACATTCGAACTAAGACATAGA 237  
  
Qy 241 CAATCCCCCAGAAATGAAACACTGAAAGTACTGAAAGTACTGAAAGTACTGAAAGTACTGAA 300  
Db 238 CAATCCCCCAGAAATGAAACACTGAAAGTACTGAAAGTACTGAAAGTACTGAAAGTACTGAA 297  
  
Qy 301 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAGATCGGCATTTTCCCAACGGG 360  
Db 298 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAGATCGGCATTTTCCCAACGGG 357  
  
Qy 361 GGTAAAGTCTGTCCACAGGATCCATGAAACAGATTTAGACAGTCTTCAGCTTATTA 420  
Db 358 GGTAAAGTCTGTCCACAGGATCCATGAAACAGATTTAGACAGTCTTCAGCTTATTA 417  
  
Qy 421 TAGATTGAGAGTGTGTGAGGAGCAGTATGGAAGCATATCGGATCTTCTGGAATCGCAT 480  
Db 418 TAGATTGAGAGTGTGTGAGGAGCAGTATGGAAGCATATCGGATCTTCTGGAATCGCAT 477  
  
Qy 481 CCTTGACACAGGGGAATATCAGGCTGGGTGAGCATCTGCCAGAGGAGAGCTTCTGCCT 540  
Db 478 CCTTGACACAGGGGAATATCAGGCTGGGTGAGCATCTGCCAGAGGAGAGCTTCTGCCT 537  
  
Qy 541 CTTTGTGACATTCGAAAGAACTTTCAGCAATTCCTCAGAGCAGCTGATCTTCTCCAGCAGAG 600  
Db 538 CTTTGTGACATTCGAAAGAACTTTCAGCAATTCCTCAGAGCAGCTGATCTTCTCCAGCAGAG 597  
  
Qy 601 AATAAAACAGAGAAGTTTCCCTGACAGAAAAGATGAAATATCTCAGAGAGACATTTGGG 660

Db 598 AATATAACAGAGAGATTTCCTGACAGAGAAAGATGAATAATCTGCAGAGAGACATTGGG 657  
Qy 661 AGAGCTGGTGAACCAATCTGTCATTTCAACAGCAATCTACATTTCAAAAGACTTGGGCAGT 720  
Db 658 AGAGCTGGTGAACCAATCTGTCATTTCAAC----- 687  
Qy 721 ATTCTAAGAAAACCGCTCAGAGAGCAAAATTCAGATGTTGCCAAGCTCTCAGTTGGCCCT 780  
Db 688 -----AGATGTTGCCAAGCTCTCAGTTGGCCCT 715  
Qy 781 TTCCTCTCACTCCTGATGACACCTCTCTCAATGAATTTCTCGATAATACTCAACGAC 840  
Db 716 TTCCTCTCACTCCTGATGACACCTCTCTCAATGAATTTCTCGATAATACTCAACGAC 775  
Qy 841 ACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTTGGAGAGCAGAGGGTG 900  
Db 776 ACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTTGGAGAGCAGAGGGTG 835  
Qy 901 GAGCTCAGCGTCTCTCTGGTAAACACAGAGTTCAAGGCAGAGCTCGCTGACTCCAGTCC 960  
Db 836 GAGCTCAGCGTCTCTCTGGTAAACACAGAGTTCAAGGCAGAGCTCGCTGACTCCAGTCC 895  
Qy 961 CCATATTACAGAGAGCTAGCAGSAAAGTCCAACTTCAGATGCAAAAAGATATTTAAGAAA 1020  
Db 896 CCATATTACAGAGAGCTAGCAGSAAAGTCCAACTTCAGATGCAAAAAGATATTTAAGAAA 955  
Qy 1021 CTTCCAGGATTCAAAAAATCCATGTTAGGATTTAGACCAAGAAAGAAAGATGGC 1080  
Db 956 CTTCCAGGATTCAAAAAATCCATGTTAGGATTTAGACCAAGAAAGAAAGATGGC 1015  
Qy 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCAGAGCAAAA 1140  
Db 1016 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCAGAGCAAAA 1075  
Qy 1141 AGCCCTGCAAGTGACCTCCTGTTTGAATTCACCAAAATTTGAAGTGAAGAGTCTAT 1200  
Db 1076 AGCCCTGCAAGTGACCTCCTGTTTGAATTCACCAAAATTTGAAGTGAAGAGTCTAT 1135  
Qy 1201 CATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCTCAGCTCAGACCTCAA 1260  
Db 1136 CATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCTCAGCTCAGACCTCAA 1195  
Qy 1261 AGGCTGATCAGAAAGCACTAGAGAGAGAAACAATCTTTGGATGTTGGGACAAATTCAGTTC 1320  
Db 1196 AGGCTGATCAGAAAGCACTAGAGAGAGAAACAATCTTTGGATGTTGGGACAAATTCAGTTC 1255  
Qy 1321 ACTGATGAATTTGTTGATCTGCCAGCTTGGTCTGACACCCCAATCAGAGCTGCC 1380  
Db 1256 ACTGATGAATTTGTTGATCTGCCAGCTTGGTCTGACACCCCAATCAGAGCTGCC 1315  
Qy 1381 ACATCTTTTGTGTTTATAACAGAGATGCTACTTTGAGTCCAGAACTTCCTCTGTTGAA 1440  
Db 1316 ACATCTTTTGTGTTTATAACAGAGATGCTACTTTGAGTCCAGAACTTCCTCTGTTGAA 1375  
Qy 1441 CCCAGCTTGACAGAGTGGAGGAGCAGAGCATGGTCTACCTGACACTCTTGGTCTCCA 1500  
Db 1376 CCCAGCTTGACAGAGTGGAGGAGCAGAGCATGGTCTACCTGACACTCTTGGTCTCCA 1435  
Qy 1501 CTTGCTATGGCTCTACCTCCTCTGTCAGAGCTCCACCTTCTTTATGGCATCAAGCATC 1560  
Db 1436 CTTGCTATGGCTCTACCTCCTCTGTCAGAGCTCCACCTTCTTTATGGCATCAAGCATC 1495  
Qy 1561 TTCCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCAAGCAATGCTAGTA 1620  
Db 1496 TTCCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCAAGCAATGCTAGTA 1555  
Qy 1621 CCAGGGCTCACCATCCACAGTGAATTTCTGCAATCAGCCAACTGGCTCTGGGAAT 1680  
Db 1556 CCAGGGCTCACCATCCACAGTGAATTTCTGCAATCAGCCAACTGGCTCTGGGAAT 1615  
Qy 1681 TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGGTC 1740  
Db 1616 TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGGTC 1675

Qy 1741 AGACACCTAGATGAATGGATCTGTGACACTCTCTGCCCATCTGAGGTACAGAGCTC 1800  
Db 1676 AGACACCTAGATGAATGGATCTGTGACACTCTCTGCCCATCTGAGGTACAGAGCTC 1735  
Qy 1801 ACGGAATATGTTCTGTCCTCCAGATCATTTCTTGAGGATACACCTCCTGTCAGCTTTA 1860  
Db 1736 ACGGAATATGTTCTGTCCTCCAGATCATTTCTTGAGGATACACCTCCTGTCAGCTTTA 1795  
Qy 1861 CAGTATATCAACACTAGTTCTATGACCAATGCCCCAAAGGCCGAGAGCTGGTAGTTC 1920  
Db 1796 CAGTATATCAACACTAGTTCTATGACCAATGCCCCAAAGGCCGAGAGCTGGTAGTTC 1855  
Qy 1921 TTCAGTCTGCGTGTGCTAAACATGSCCTTCTCCACGACCTGTTCAACAAGAGCTCTCTG 1980  
Db 1856 TTCAGTCTGCGTGTGCTAAACATGSCCTTCTCCACGACCTGTTCAACAAGAGCTCTCTG 1915  
Qy 1981 GAGTACCCAGAGCTCTGGAGCAACAATTCACAGAGTGTCTGTTTCCATATCTACGATCCAAT 2040  
Db 1916 GAGTACCCAGAGCTCTGGAGCAACAATTCACAGAGTGTCTGTTTCCATATCTACGATCCAAT 1975  
Qy 2041 CTTACAGAGTTTAAGCAACTTGAATACTTAACCTTCAGAAAACGGAGTGTGATTTGAAT 2100  
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Db 2036 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGGTATAACCTCACAAAGGCTGTGCACGGGTC 2095  
Qy 2161 TTGAGGATTTTCTGTTCTGCTGAGCCCAACAACCTCCATCTGGAATAAGACAGTACTCT 2220  
Db 2096 TTGAGGATTTTCTGTTCTGCTGAGCCCAACAACCTCCATCTGGAATAAGACAGTACTCT 2155  
Qy 2221 CTCACATTTGAACACAGCTGATCAAGCAGATCCCTGCAAGTTCCTGGCTCGCGCAATTT 2280  
Db 2156 CTCACATTTGAACACAGCTGATCAAGCAGATCCCTGCAAGTTCCTGGCTCGCGCAATTT 2215  
Qy 2281 GCCCAATGTGTAAGAACGAAACGGAAGCTGAGAAAGCGGAGTGTGCTGCAAAACAGGATAT 2340  
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Qy 2341 GACAGCCAGGGAGCTGAGCGGTCTGGAACAGGCTCTGTGGCCCTGGCCACAAAGGAA 2400  
Db 2276 GACAGCCAGGGAGCTGAGCGGTCTGGAACAGGCTCTGTGG--CCTGGCACAAGGAA 2334  
Qy 2401 TCCGAGGCTCTCCAGGAAAGGGAGCTCCATGCGAGTTCAGAGATCACTCTGAAAAATCAA 2460  
Db 2335 TCCGAGGCTCTCCAGGAAAGGGAGCTCCATGCG--GGTTCCAGATCACTCTGAAAAATCAA 2392  
Qy 2461 GATACAAAACCTAGTGTGTTAAAGTTCCAAAATCAAAATAACAGGTTAATCAGTAAA 2520  
Db 2393 GATACAAAACCTAGTGTGTT--AAAAGTTCCAAAATCAAAATAACAGGTTAATCAGTAAA 2451  
Qy 2521 AGAAATCTGAAATTAAGCGTAGAATATGAAGAATTTAAACCAAGATTGGAAGGA 2580  
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Qy 2581 AATTAATACTGAAATGTACAAATTAATCACTTAGGCTATCTCAAGAGAGATGATTTGGCT 2640  
Db 2512 AATTAATACTGAAATGTACAAATTAATCACTTAGGCTATCTCAAGAGAGATGATTTGGCT 2571  
Qy 2641 TCTCAAGGAAATGAGACAGGATTTATCATGGGTATCAAAATCCAGACATACAGTCAA 2700  
Db 2572 TCTCAAGGAAATGAGACAGGATTTATCATGGGTATCAAAATCCAGACATACAGTCAA 2631  
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Db 2632 CACTGAGATCAGACACACCATATTTCAAAATATAGAAGATGATGTTACTTGGCAACAG 2691  
Qy 2761 TAAATTCGAAAAAAGACACACTTATTTAATAACCCCAATGCAATCAGCGAAGAC 2820  
Db 2692 TAAATTCGAAAAAAGACACTTACTTATTTAATAACCCCAATGCAATCAGCGAAGAC 2751



QY 1596 GGCACCTGACGAGACAATGCTAGTACAGGGCTCACCATCCCCACAGTGATTAATCTGCG 1655  
DB 1153 GGCACCTGACGAGACAATGCTAGTACAGGGCTCACCATCCCCACAGTGATTAATCTGCG 1212  
QY 1656 AATCAGGCAACTGGCTCTGGGAATTTTCCATCCACCTGCAATCTTCAGATCAGACGCGGATC 1715  
DB 1213 AATCAGGCAACTGGCTCTGGGAATTTTCCATCCACCTGCAATCTTCAGATCAGACGCGGATC 1272  
QY 1716 AAGTGCAGGTGGGGAAGATATGCTGACAGACCTAGATGAATGGATCTGCTGACACTCC 1775  
DB 1273 AAGTGCAGGTGGGGAAGATATGCTGACAGACCTAGATGAATGGATCTGCTGACACTCC 1332  
QY 1776 TGCCCCATCTCAGGTACAGAGCTCAGCAATATGTTTCTGCCAGATCATTTCTTGA 1835  
DB 1333 TGCCCCATCTCAGGTACAGGGCTCAGCAATATGTTTCTGCCAGATCATTTCTTGA 1392  
QY 1836 GGATACCACTCTCTCAGCTTACAGTATATCACCACCTAGTCTATGACCAATTCGCC 1895  
DB 1393 GGATACCACTCTCTCAGCTTACAGTATATCACCACCTAGTCTATGACCAATTCGCC 1452  
QY 1896 CAAGGCGGAGAGCTGGTGTCTTTCAGTCTGCGGTGTTCTAAATGCGCTTCTCCAA 1955  
DB 1453 CAAGGCGGAGAGCTGGTGTCTTTCAGTCTGCGGTGTTCTAAATGCGCTTCTCCAA 1512  
QY 1956 CGACCTGTTCACCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAAATTCACAGCT 2015  
DB 1513 CGACCTGTTCACCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAAATTCACAGCT 1572  
QY 2016 GCTGGTTCATATCTAGATCCATCTTACAGATTTTAAAGCACTTGAATCTTAACT 2075  
DB 1573 GCTGGTTCATATCTAGATCCATCTTACAGATTTTAAAGCACTTGAATCTTAACT 1632  
QY 2076 CAGAAACGGGAGTGTGATGTGAATAGCAAAATGAAGTTTCTGAAGTCTGCGGTATAA 2135  
DB 1633 CAGAAACGGGAGTGTGATGTGAATAGCAAAATGAAGTTTCTGAAGTCTGCGGTATAA 1692  
QY 2136 CCTCACAAGCTGTGACAGGGGTCTTGGAGGATTTTCGTCTGCTGAGCCCAACACT 2195  
DB 1693 CCTCACAAGCTGTGACAGGGGTCTTGGAGGATTTTCGTCTGCTGAGCCCAACACT 1752  
QY 2196 CCATCTGGAATAGACAGCTACTCTCTCAATTTGAACAGAGTGTATCAAGCAGATCCCTG 2255  
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QY 2256 CAAGTTCCTGCGCTGCGGGAATTTGCCAATGTGTAAAGAACGAACTGAGGAAGC 2315  
DB 1813 CAAGTTCCTGCGCTGCGGGAATTTGCCAATGTGTAAAGAACGAACTGAGGAAGC 1872  
QY 2316 GGAGTGTGCTGCAACACGAGATATGACAGCGGAGCTGAGCGGTCTGGAACGAG 2375  
DB 1873 GGAGTGTGCTGCAACACGAGATATGACAGCGGAGCTGAGCGGTCTGGAACGAG 1932  
QY 2376 CCTCTGTGGCCCTGGCAAGGAATGCGAGGTCTCTCAGGGAAGGGAGCTCCATGCGAG 2435  
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DB 1993 GTTCCAGATCAGTCTGAAATCAAGCATACAAAATAGTGTAAAGTTTCAAATCA 2052  
QY 2496 ACAAATTAACAGGTAATCAGTAAAGAAATTTCTGAATTTACTGACCGCTAGAAATGAAGA 2555  
DB 2053 ACAAATTAACAGGTAATCAGTAAAGAAATTTCTGAATTTACTGACCGCTAGAAATGAAGA 2112  
QY 2556 ATTTAAACATCAAGATTGGGAAGAAATTTAAATCTGAAATGTACAAATTTACATTAGG 2615  
DB 2113 ATTTAAACATCAAGATTGGGAAGAAATTTAAATCTGAAATGTACAAATTTACATTAGG 2172  
QY 2616 CTATCTCAAGAGATGATTTTGCCTTCTCAAGGAAATGGAGCAGGCATATTTCATGGGT 2675  
DB 2173 CTATCTCAAGAGATGATTTTGCCTTCTCAAGGAAATGGAGCAGGCATATTTCATGGGT 2232

QY 2676 CATCAAAATCCAGACATACAGTCAACCTGAGATCAGCACACCATATTTTCAATATA 2735  
DB 2233 CATCAAAATCCAGACATACAGTCAACCTGAGATCAGCACACCATATTTTCAATATA 2292  
QY 2736 GAAAGAGTCAATGCTACTTGGCAACCAAGTAAATTTCTGAAAGAAAGACACTTACTTATTATA 2795  
DB 2293 GAAAGAGTCAATGCTACTTGGCAACCAAGTAAATTTCTGAAAGAAAGACACTTACTTATTATA 2352  
QY 2796 AAACCCCAATGCAATCAGCGAAACATATTTTACTATTCTTGGATGATAGTCAAAATGA 2855  
DB 2353 AAACCCCAATGCAATCAGCGAAACATATTTTACTATTCTTGGATGATAGTCAAAATGA 2412  
QY 2856 TCATAAGCCAGGTTTGTCTTCCACCTTCCCTGAAATTTTACTCACAGATCATTTTGCACA 2915  
DB 2413 TCATAAGCCAGGTTTGTCTTCCACCTTCCCTGAAATTTTACTCACAGATCATTTTGCACA 2472  
QY 2916 AGCATAGCTTACTTATTTAGGACCTGAACAAATTTTATTTGGGAAGCAACTCTTTATAT 2975  
DB 2473 AGCATAGCTTACTTATTTAGGACCTGAACAAATTTTATTTGGGAAGCAACTCTTTATAT 2532  
QY 2976 GCTAGAAAGTACATTTAAAGATGACTTACCGAGGAGATGAGGTCTCTCTAAACG 3035  
DB 2533 GCTAGAAAGTACATTTAAAGATGACTTACCGAGGAGATGAGGTCTCTCTAAACG 2592  
QY 3036 CATGAATGTATGTAGTGTGTAGGCACTGTAGTGTATATATGCTCCACACTACGTCT 3095  
DB 2593 CATGAATGTATGTAGTGTGTAGGCACTGTAGTGTATATATGCTCCACACTACGTCT 2652  
QY 3096 GATAAACCAAACTCAGTATTTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGCG 3155  
DB 2653 GATAAACCAAACTCAGTATTTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGCG 2712  
QY 3156 TTACATAGTACAGTCTTTTGTGCAATAATCTTTGAATGTTCTTTTAAAGAACTATTTT 3215  
DB 2713 TTACATAGTACAGTCTTTTGTGCAATAATCTTTGAATGTTCTTTTAAAGAACTATTTT 2772  
QY 3216 GTTCAGATACATACATACCTGAGAAATCTTACTTTCTTGTACTACACAAGCTATTTT 3275  
DB 2773 GTTCAGATACATACATACCTGAGAAATCTTACTTTCTTGTACTACACAAGCTATTTT 2832  
QY 3276 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATGACATAATCAAT 3330  
DB 2833 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATGACATAATCAAT 2887

## RESULT 4

US-10-007-270-5  
; Sequence 5, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hagaman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 2244  
; TIPS: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(2244)  
; OTHER INFORMATION: n is a, c, g, or t.







QY	2101	AGCAAAATGAAGTTTGGCTTAAGTCTGTGCCGTATAA	CCTTACCAAGGCTGTGCAAGGGGTC	2116
DB	2120	AGCAAAATGAAGTTTGGCTTAAGTCAAGTGTAA	CCTTACCAAGGCTGTGCAAGGGGTC	2179
QY	2161	TTGAGGATTTTCGTTCTGCTGCAGCCCAACAACT	CCCATCTGGAATAGACAGCTACTCT	2220
DB	2180	TTGAGGATTTTCGTTCTGCTGCAGCCCAACAACT	CCCATCTGGAATAGACAGCTACTCT	2239
QY	2221	CTC	2223	
DB	2240	CTC	2242	

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RESULT 5
US-10-007-270-8
; Sequence 8, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3668
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform A
; NAME/KEY: misc feature
; LOCATION: (1)-(3668)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-8

Query Match          41.3%; Score 1375.6; DB 13; Length 3668;
Best Local Similarity 70.7%; Pred. No. 0;
Matches 217; Conservative 1; Mismatches 730; Indels 169; Gaps 19;

QY      1  TAAACCAAGAGGTTATCCTCAATCACTCGTATCAATATATATATATTTTTCACATTTC 60
DB      62  TAAACCAAGGAGGTCGTCTACTCAGCGGCACCTGGATTGATTATTTTTCATATTC 121
QY     61  TGTACTTTTT-----AATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATACC 113
DB     122  AGTCACCTTATTTCTTTAAGTGTGACTTGGTATTGTTCTGTGATTTT-TCAGAATTACC 179
QY     114  AATGCCAAAGCCAGAAATGATTGGAACACTAGAAGCTATTTTGTGTTTTTGGATTT 173
DB     180  AGTATACAGAA-CAGAAATGAATTTTCAAAATAAACATGCTATCTTTGTTTTTGGGATTT 238
QY     174  TTCTCCAAAGTTCAGGAACCAAGATATCTCATTAAACATATACCATCTGAAACTAAAG 233
DB     239  TTCTCCAAAGTTCAGGAATCAAGATACCCTATTAAATATTCAGTTCGAATTAATAA 298
QY     234  ACATAGACAATCCCCCAGAAATGAACCACTGAAAGTACTGAAAAAATGTACAAAATGT 293
DB     299  ACATAGACAAACCCCAAGATTCGAACAAATTTGAAGTACTTTCACAGTGCACAAAGTGT 358
QY     294  CAACTATGACAGCAATATTCGATTTTGGCAAGCATCGAACAAAAAGATCCGCATTTTTCC 353
DB     359  CAACCATGAACGAATATTCGATTTCGCAAGCTTCGAACCAAAAGATTCAGCACTTTTCC 418
QY     354  CAACGGGGGTTAAAGTCTGTGCCAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAG 413

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Db	419	CA---GCTGCTAACATCTCTGCACAGGAATCCTTGAGACAGATTTTATAGCAAGTCTTCAAG	475
Qy	414	CTTATTATATAGATTGAGAGTGTGTACAGAAAGCATATGGGAAGCATATCGATATCTTTCTGG	473
Db	476	AATATTATATAGATGTGAGATATGTCTAAGAAAGTCTGTGGGAAGCATATCGTATCTTTCTGG	535
Qy	474	ATCGCATCCCTGCACACAGGGGAATATCAGACATGGGTTCAGCATCTGCCACAGAGACCT	533
Db	536	ACCGAATTCCTGCACACAGAGGAATATCAGACTGGGTTCAGCCTCTGCCAGAAAGAACCT	595
Qy	534	TCTGCCTCTTTGCATTTGGAAAAAATCTCAGCAAAATCCACAGGAGCACTCGGATCTTCTCC	593
Db	596	TCTGCCTCTTTGCATTTGGAAAAAATCTCAGCAAACTCCACAGGAGCACTAGATCTTCTTC	655
Qy	594	AGCAGAGAATAAACACAGAGAGTTCCTCTGCACAGAAAGATGAAATATCTGCAGAGAGA	653
Db	656	AGCAGAGATAAACACAGAGAGTTCCTCTGGGAGGAAGATGAGACAGCCTCCATGGAGA	715
Qy	654	CATTGGAGAGCCTGTGTGAAACCAATTTGTCATTTCACAGCAATCTACATTTCAAAGACTT	713
Db	716	CACCTGGAAGCACCTACTGGAAGCCCTGTGTACCCAC	752
Qy	714	GGGCAGTATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTGGCCAACTCTCACT	773
Db	753	-----AGATGTTTCCAGGATGTCCCT	773
Qy	774	TGGGCTCTTCCCTCTCACTCCCTGATCACACCCCTCCTCAATGAAATTTCTGATATACTACCT	833
Db	774	GGGGCCCTTCCCACTTCCCTCTGATGCACAGACCTCAGGAGATTTCTCAGTGTCACTCT	833
Qy	834	CAACGACACAAGATGCTTACAAACAGAAAGAGAAAAAGAA-----TTGCTGT	881
Db	834	CAAGGACATTTCAAAGCCCAACACACAGAAAGTAAACAGAAACCTATTCACTGTCTGAATT	893
Qy	882	GTGGAGGAGCAGAGGTTGGAGCTCAGCGTCTCTCTGTAAACACAGAAATTCAGAGGAGA	941
Db	894	CTCATCAGAGGAGAGGTGGAAATTCAGCATCTCTCTGCCAAACCAACAGGTTCAAGGCAGA	953
Qy	942	GCTCGTGACTCCAGTCCCAATATTACCAGGAGCTAGCAGAAAGTCCCAACTTTCAAT	1001
Db	954	GCTCACCAACTCTGGGTCCACATATACCAGGAACCTGGTGGGACAGTCCCAACTGCGAGTT	1013
Qy	1002	GCAAAAGATTTTAAAGAACTCCAGGATTTCAAAAAATCCATGTGTAGATTTAGACC	1061
Db	1014	GCAAAAGATTTTAAAGAACTCCAGGATTCGGAGAAATCCGTGTATTAGATTTAGACC	1073
Qy	1062	AAAGAAAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGSCCATCTTTAAGAG	1121
Db	1074	AAAGAAAGAGAGATGGTTCAAGCTCCACAGAAATACAGCTTATGSCCATCTTTAAGAG	1133
Qy	1122	ACACAGTGCAGAGCAAAAAGCCCTGCAGTGAACCTCTGTCTTTTGATTTCCACAAAT	1181
Db	1134	GGACCATGCAGAGCAAAAAGCCCTGATAGTCACTCTCTCTTGATTTCCACAAAT	1193
Qy	1182	TGAAGTGGGAAGTCTATCATGGAACCATGGAGGAGGAACAAGCAACCGAAATCTATCT	1241
Db	1194	TGAAGTGAAGAAATCCATCATGAGTCAAGAA--GACAAACACCAAGAACTACCT	1250
Qy	1242	CACAGCTACAGACCTCAAAAGGTGTATGACGAAGCACTAGAGAGAGAAACAATCTTTGGA	1301
Db	1251	CACAGCTACAGACCTCAAAAAAATCTCATATCAACACTAGATGGAGACCTGCTCTTGGT	1310
Qy	1302	TGTGGGACAAATTCAGTTCACTCATGAAATGCTGGATCACTGCCACCTTTGGTCTCTGA	1361
Db	1311	AGAAGGGAAGAAATTCATTCGGTGATGAAGTTACTGGGACACT-----CTTCAGACCTGT	1364
Qy	1362	CACCCATCAGAGCTGCCCAATCTTTTGTGTATTAAACAGAGATGCTACTTTTGTGCTCC	1421
Db	1365	CACCTGAACAGATCTGCCCCAAGCCCTTGCTGATGTACAGAGAGATGCCACTTTTGTGCTCC	1424
Qy	1422	AGAACTCTCTCTTTGAACCCAGCTTTGAGACAGTGGACGGACGACGATGGTCTTACC	1481
Db	1425	AGAACTCTCTCTCTTTGAGCCTTAGGCTTTAGGCAGTGGACAGAGAGGAATCTGAGCTGCC	1484

QY 1482 T-----GACACTTCTGGTCTCCACCTGCTATGCGCTCTACCTCCCTGTC 1526  
Db 1485 TGGATGCTCTCAAGACAGTTCCTGGTCTCCACCTGATACAGCTCAATTTCCCGATC 1544  
QY 1527 AGAAGCTCCACCTTTCTTTATGGCATCAAGCATCTCTCTCTGACTGATCAAGGCACAC 1586  
Db 1545 AGAAATCTACCTTCGTTTA--CACTAGCATCTCTCTCTAGATGCTCAAGCCCCC 1601  
QY 1587 AGATACATGGCACTGACACAGCAATGTAGTACAGGGCTCACCATCCCAACAGTGA 1646  
Db 1602 TCCTTGATGACCACTGGCCCAACAGCACTCAATCCCAAGCCCACTCTCCCACTATCGA 1661  
QY 1647 TTATTCGCAATCAGCCAACTGCTCTGGGAAATTTCACATCCACCTGCATCTTCAGATCA 1706  
Db 1662 TTATTCATCATCCGCCAATTCCTCTGNAATCGTCAATTCGCTGCACTCTCCAGTGA 1721  
QY 1707 CAGCGATCAAGTGCAGGTGGGAAATATGTCAGACACCTAGATGAATGATCTGTC 1766  
Db 1722 CAGAGAGCTGATCACAAGCAGCCATGACAAATCCGAGACCTAGATGGCATGGATGTC 1781  
QY 1767 TGACACTCCTGCCCATCTGAGTACCAGAGCTCAGGATATGTTTCTGCCGATCA 1826  
Db 1782 TGACAGCCAGCTTGTGCAAAATATCAGAACTGAGTGGATGATCTTCGCTCGGCTCA 1841  
QY 1827 TTTCTTGGAGATACCACTCCTGCTCAGCTTTACAGTATATCACCACCTAGTTCTATGAC 1886  
Db 1842 GTTCTTGGAGATGACACACCCATCCCAACAGTACGTTTCATCACCACCACTCCGAGAC 1901  
QY 1887 CATTCGCCCAAGGCGGAGAGCTGTTAGTGTCTTCAGTCTGCGTGTGCTAAATGCG 1946  
Db 1902 CATTCGCCCAAGGCGGAGAGCTGTTAGTGTCTTCAGCTGCGTGTGCTAAATGCG 1961  
QY 1947 CTTCTCCCAAGCACTGTTCAACAAGAGCTCTCGAGTACCGAGCTCTGAGCAACAAT 2006  
Db 1962 GTTCTCTGATGACTGTTCAACAAGAGTCTCTGAGTATCAGCCCTGGAACAAGATT 2021  
QY 2007 CACAGAGCTGCTGGTTCATATACGATCCAACTTACAGGATTTAAGCACTTGAAT 2066  
Db 2022 CACAGAGCTGCTGGTTCATATACGATCCAACTTACAGGATTTAAGCACTGGAAT 2081  
QY 2067 ACTTAATCTCAGAAACGGAGTGTGATGATGCAATGCAAAATGAATGCTTGAATCTGT 2126  
Db 2082 ACTCAGCTTCAGAAACGGAGTGTGATGATGCAAAATGAATGCTTGAATGCTTGAATGCT 2141  
QY 2127 GCGGTATTAACCTCACCAGGCTGTGACGCGGTCTTGGAGGATTTTCTGCTGCGAGC 2186  
Db 2142 ACCCTACAACTCACCAGGCGGTGCGCGGTCTTGGAGGATCTCGTCCACCGCAGC 2201  
QY 2187 CCAACAACTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAAGC 2246  
Db 2202 TCAAGGCTCAATCTGGAATCGAAAGCTACTCCCTCGACATTTGAACAGCTGATCAGC 2261  
QY 2247 AGATCCCTGCAAGTCTCTGCGCTGCGGCAATTTGCCAATGTGTAAGAAACGAACGGAC 2306  
Db 2262 GGATCCCTGCNAACTCTAGACTGTGGCAATTTGCCAGTGTGTAAAGATGATGGAC 2321  
QY 2307 TGAGGAAGCGGAGTGTGCTGCAAAACAGGATATGACACCGGGAGCGCTGGAAGTCT 2366  
Db 2322 AGAGGAAGCAGAGTGTGCTGCAAAACAGGATATGACACCGGGAGCGCTGGAAGTCT 2381  
QY 2367 GGAACAGGCGCTGTGCGCTGCGCAAGGATTCGAGGTCTCTCAGGGAAGGGAGC 2426  
Db 2382 GACCTTGAACTCTGCTCCCTGG---AAGACTTGTGTGGCGCGCGAGAACAGCAAC 2438  
QY 2427 TCCATGAGGTTGCCAGATCACTCTGAAATCAAGCATACAAACTAGTGTGTTAAAGTT 2486  
Db 2439 TCCATGAGGTTGCCAGATCACTCTGAAATCAAGCATACAAACTAGTGTGTTAAAGTT 2498  
QY 2487 CCAAAATCAACAAATTAACAGTATTCAGTAAAGAAATTTGAAATTTACTGACCGTGA 2546  
Db 2499 ACCTGACGAA-----AATAGGTAGTCAAGAAAGAAATTTCTAACTATCATGCTATAGG 2552

QY 2547 ATATCAGAAATTTAACCATCAAGATTCGGAGGAATTTAAAACTGAA----- 2595  
Db 2553 ATTTCAAGATTTGAAGACCCAGGACTGGAGGAAATTTAAAGCTGGAATCATATGCAATT 2612  
QY 2596 -----ATGTACAATTTATCATTACCTTAGGCTATCTCAAGAGAGATGATTTGCT 2640  
Db 2613 ATGTTGCAAACTCTGTTGAAAGGAACTTTTATTTCTTTAAAGAAAGTGTATCTGTTCTGT 2672  
QY 2641 TCTCAGGAAATGGAGACAGGCATATTCATGGGTCAATCAAAATCCAGACATACAGTCAA 2700  
Db 2673 TAACCTTCGAAAAACAGAGGGAGAGATTCAGTGTCTATTTGGAATACAGGCATGTAATCAA 2732  
QY 2701 CACTGAGAAATCAGCACACACCATATTTCAAAATATAGAGAGTCAATGTACTTGGCAACCCAG 2760  
Db 2733 CTTTGAGACTCAG-----CATGCTTGAACAAGACAGCAGGCGTGTATTTGTATGA-CAG 2784  
QY 2761 TAAATTCGAAAAAAGACACTTACTTATTTATTA--AAACCCCAATGCAATCAGCGAA 2818  
Db 2785 TTAAGCCTGTTGGGGGGGGGACATATTTTGTAGTCAAACTCAAGCAATCATTTGA 2844  
QY 2819 ACATATTTTACTTCTTGGATGATAGTCAAAATGATCATAGCCAGGTTTGTCTCCAC 2878  
Db 2845 ACACA-TTGTGCTATTTTGGACAGTACTC--AAGTAGCAAGATAAGGTTAGCTTTTTT 2901  
QY 2879 CTTCCCTGAAATTTTACTCAGATCATTTTGCACCAAGCATAGCTTACTTATTTGTTAG 2938  
Db 2902 CTTTCTTTAAATTTATACATAAARCTTATTTCAAAATAAATACAACT-----TTGTTTAG 2954  
QY 2939 GGACTGCAACATTTTGGGAGCAAACTCTTATATGCTTAGAAGTACATTTAAAGAT 2998  
Db 2955 TGGGTGTACAATATGAGGATCTGATTTCTTTATATGTTAGATATACAGTTAAAGAT 3014  
QY 2999 CACTACTTACGC 3010  
Db 3015 TATCATTTGGGC 3026

## RESULT 6

US-10-007-270-10  
; Sequence 10, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 1726  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D  
US-10-007-270-10

Query Match 16.0%; Score 534; DB 13; Length 1726;  
Best Local Similarity 72.0%; Pred. No. 1.4e-133;  
Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;  
QY 396 TTTTAGACAGTCTTCAAGCTTATATAGATGAGGTGTCAGGAGCAGTATGGGAAG 455  
Db 171 TTTTGGGATTTTCTCCAAAGTTCAGGAATCAAGTATGTCAGAAAGTCTGTTGGGAAG 230  
QY 456 CATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGACTGGGTACGA 515

Db 231 CATATCGTATCTTTCTGGACCGAATTCTCTGACACAGAGGAATATCAAGACTGGGTGAGCC 290  
Qy 516 TCTGCCAGCAGGAGACCTCTGCTCTTTGACATTGGAAAAAATTTTTCAGCAATTCCTCAGG 575  
Db 291 TCTGCCAGAAAGAACCTTCTGCTCTTTGACATTGGGAAATTTTTCAGCAATTCCTCAGG 350  
Qy 576 AGCACTGGATCTTCTCCAGCAGAGATATAAAGAGAGATTTTCCCTGACAGAAAGATG 635  
Db 351 AGCACTGATCTTCTTTCAGCAGAGATATAAAGAGAGATTTTCCCTGAGGAGAAAGATG 410  
Qy 636 AATATCTGAGAGAGACATTTGGAGAGCTGGTGAACCATTTGTCATTTCACAGCAA 695  
Db 411 AGCAGCTCTCATGGAGACATCTGAAGCCTACTGAAGCCCTGTGTACCCAC----- 465  
Qy 696 TCTACATTTCAAGACTTGGGAGATTTCTAAGAAACCTCTGAAGAGCAATTCAGAA 755  
Db 466 -----AGG 468  
Qy 756 TGTGGCAACGCTCACTTGGGCTTTCCCTCTCACTCTGATGACACCTCTCAATGA 815  
Db 469 TGTTCAGAGATGTCCTTGGGCTCATTTCCACATTTCTTCTGATGACAGACCTCAAGGA 528  
Qy 816 AATCTCGATTAATCACTCAACGACCAAGATGCTTACACAGAAAGAGAAACGAA-- 873  
Db 529 GATCTCAGTCTACCTCTCAAGGACATTTCAAAAGCCCAACAGAAAGTATACAGAAC 588  
Qy 874 -----TTCTGCTGTGTGGAGGACAGAGGTGGAGCTCAGCGTCTCTGTGTAA 923  
Db 589 TATTCAGTGTCTGAATTTCTCATCAGAGGAGAGGTGGATTCAGCATCTCTCTGCCAA 648  
Qy 924 CCAGAGTTTCAAGCAGAGCTCGGTGCTCCAGTCCCTCATTTTACCAGAGCTAGCAGG 983  
Db 649 CCAGAGTTTCAAGCAGAGCTCACCACCTCTGGGTCACTACTACAGGAACTGGTGG 708  
Qy 984 AAGTCTCACTCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAGAAATTCGA 1043  
Db 709 ACAGTCTCACTGAGTTGCAAAAGATATTTAAGAACTTCCAGGATTCGGGAAATCCG 768  
Qy 1044 TGTGTAGGATTTAGCAAAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACT 1103  
Db 769 TGTATAGGATTTAGCAAAAGAAAGAAAGATGGTTCAGCTCCACAGAAATACAGCT 828  
Qy 1104 TACGGCCATTTTAAAGACACAGTGAGAGCAAAAGCCCTGCAAGTCACTCTCTGTC 1163  
Db 829 TATGGCCATCTTAAAGAGGACCATGCAAGAGCAAAAGCCCTGATAGTCTATCTGTC 888  
Qy 1164 TTTGATTCGAACCAAAATTTGAAGTGAAGATTTTGAAGTGAAGTCCATCATGGAGTCA 945  
Db 889 TCTTGAATTCGAACCAAAATTTGAAGTGAAGATTTTGAAGTGAAGTCCATCATGGAGT 1283  
Qy 1224 GCAACAGAAATCTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGAAAGCACTAGA 1283  
Db 946 ACAACAGAAACCTTACCTCAGAGCTACAGACCTCAAAAGGCTGATCAGAAAGCACTAGA 1005  
Qy 1284 GGAAGAACTTTTGGATGTTGGGACATTTCACTGATCAATTTCTGATCACT 1343  
Db 1006 TGGAGACCTGTCTTGGTAGAGGAAATTTCCATTCGGTGAATGATGATTTCTGGGACCT 1065  
Qy 1344 GCCAGCTTTGCTGCTGACACCCATCAGAGCTGCCACATCTTTTGTGTATTAACAGA 1403  
Db 1066 -----CTTCAGACTGTCTGATGACACAGATCTGCCAGGCCCTTGTGTATTAACAGA 1119  
Qy 1404 GATGCTCTTTTGGATGTTGGGACATTTCACTGATCAATTTCTGATCACT 1463  
Db 1120 GATGCCACTTTTGGATGTTGGGACATTTCTTCTGTTGAAACCCAGCTTGGAGAGTGGACG 1179  
Qy 1464 AGCAGAGATGCTGTACCTG 1483  
Db 1180 AGAAGATCTGAGTGGCTG 1199

RESULT 7

US-10-007-270-12

; Sequence 12, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 1321  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform E  
; US-10-007-270-12

Query Match 14.8%; Score 491.6; DB 13; Length 1321;  
Best Local Similarity 76.0%; Pred. No. 3.8e-122;  
Matches 634; Conservative 1; Mismatches 190; Indels 9; Gaps 2;  
Qy 1767 TGACACTCTGCCCATCTGAGTACCAGAGCTCAGCGAATATCTTCTGTCCTCCAGATCA 1826  
Db 319 TGAACCGCGCCCTGTTCAGAAATATCAGAACTCAGTGGATACGATTTCTGCTCGGTCA 378  
Qy 1827 TTTCTTGGAGATACCACTCTCTCAGCTTTTACAGTATATCACCACTAGTTCTTATGAC 1886  
Db 379 GTTCTTGGAGATGACCAACCCATCCCAACAGTAGTACGTTTCATCACCACTCCGAGAC 438  
Qy 1887 CATTGCCCCCAAGGGCCGAGAGCTGTGTAGTGTCTTCTCAGTCTGGTGTGTGTAACATGC 1946  
Db 439 CATTGCCCAAGGGCCAGAGCTAGTGTGTATCTTACGCTGCTGTGTGTAAATGCC 498  
Qy 1947 CTTCCTCAACGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAT 2005  
Db 499 GTTCTCTATGACCTGTTTCAACAGAGTCTCTGGAGTATCAAGCCCTGGAAACAGATT 558  
Qy 2007 CACAGAGCTGTGTTCCATATCTACGATCCAAATCTTACAGATTTAAGCAACTTGAAT 2065  
Db 559 CACAGAGCTGTGTTCCATATCTACGATCCAAATCTTACGAGTATTAAGCAACTTGAAT 618  
Qy 2067 ACTTAACCTCAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTTGTAACTCTGT 2126  
Db 619 ACTCAGCTTCAAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTTGTAACTCTGT 678  
Qy 2127 GCCGTATAACCTCACCAGGCTGTGCACGGGTCTTGGAGATTTTCTGTCGACG 2186  
Db 679 ACCCTACACCTCACCAGGCTGTGCACGGGTCTTGGAGATTTTCTGTCGACG 738  
Qy 2187 CCAACAACTCCTCTGGAATAGACAGCTACTCTCTCAACATTTGAACCAAGCTGATCAAGC 2246  
Db 739 TCAGGGCTCAATCTGGAATTCGAAGTACTCTCCCTCGACATTTGAACCAAGCTGATCAAGC 798  
Qy 2247 AGATCCCTCAAGTTCCTGCGCTGCGGCAATTTGCCCAATGTGTAAAGAACGACGAC 2306  
Db 799 GATCCCTGCAACTCTAGACTGTGGCAATTTGCCCAAGTGTGTAAAGAACGACGAC 858  
Qy 2307 TGAGGAGCGAGTGTGCTGTGAAACCAAGGATATGACAGCCAGGGAGCTTGGAGCTCT 2366  
Db 859 AGAGGAGCAGAGTGTGCTGTGAAACCAAGGATATGACAGCCAGGGAGCTTGGAGCTCT 918  
Qy 2367 GGAACCCAGGCTCTGTGGCCCTGGCAAAAGGATGCGAGGTCTCTCCAGGGAAGGGAGC 2426  
Db 919 GACCTTGAACCTCTGTCCCTCTGG---AAGACTTGTGTGGCCGCGCGAGCAAGCAAC 975  
Qy 2427 TCCATGCGAGTTGCCAGATCACTCTGAAATTCAGCATACAAACTAGTTTAAAAAGTT 2486

Db 976 TCCATGAGCCACAGATCCTCTACAAACCAAGCTCAGAACCTGGTGTAAAAAGCT 1035  
QY 2487 CCAAAATCAACAAATTAACAGGTAATCACTAGTAAAGAAATTTCTGAATTAATCTGACCTAGTA 2546  
Db 1036 ACGTCAGCAA-----AATAAGGTAGTCAAGAAACGAAATCTTAAACTATCAGCTATAGG 1089  
QY 2547 ATATGAAGATTTAAACCATCAAGATTCGGAGGAAATTAATAAATCTGAAATGTA 2600  
Db 1090 ATTGAAATTTGAAGACCAAGGACTGGAGGAAATTTAAAGCTGAATCATA 1143

RESULT 8  
US-10-007-270-14  
; Sequence 14, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Monkey IPM 150 cDNA (partial)  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Monkey species  
US-10-007-270-14

Query Match 13.2%; Score 439; DB 13; Length 555;  
Best Local Similarity 85.8%; Pred. No. 3.8e-108;  
Matches 526; Conservative 0; Mismatches 25; Indels 62; Gaps 1;

QY 347 TTTTCCCAACGGGGTTAAAGTCTCTCCACAGGAATCCATGAAACAGATTTTAGACAGT 406  
Db 4 TTCTTTCCGAACGGGGTTAAAGTCTCTCCACAGGAATCCATGAAACAGATTTTAGCCAGT 63  
QY 407 CTTCAAGCTTATTATAGATTGAGTGTCTCAGGAAGCAGTATGGGAAGCATATCGGATC 466  
Db 64 CTTCAAGCTTATTATAGATTGAGTGTCTCAGGAAGCAGTATGGGAAGCATATCGGATC 123  
QY 467 TTTCTGGATCGCATCCCTGCACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAG 526  
Db 124 TTCTCTGGATCGCATCCCTGCACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAG 183  
QY 527 GAGACCTTCGCTCTTTGACATTTGAAAATCTTCAGCAATTCAGGAGCAGCTGGAT 586  
Db 184 GAGACCTTCGCTCTTTGACATTTGAAAATCTTCAGCAATTCAGGAGCAGCTGGAT 243  
QY 587 CTTCTCCAGCAGAGATAAACAAGAGAGTTCCTCTGACAGAAAAGATGAATATCTGCA 646  
Db 244 CTTCTCCAGCAGAGATAAACAAGAGAGTTCCTCTGACAGAAAAGATGAATATCTGCA 303  
QY 647 GAGAAGACATTGGGAGGCTGGTGAACCAATGTTCATTTCAACAGCAATCTPACATTTCA 706  
Db 304 GAGAAGACATTGGGAGGCTGGTGAACCAATGTTCATTTCAACAGCAATCTPACATTTCA 347  
QY 707 AAGACTTGGCAGTATTCTAAGAAACCCCTCAGAGAGCAATTCAGATGTTGCCAAGC 766  
Db 348 -----AGATGTTGCCAGC 361  
QY 767 TCTCACTTGGGCGTTTCCCTCTCACTCTCTGATGACACCCCTCTCAATGAAATTTCTCGATA 826

## RESULT 9

US-10-027-632-286848/c  
; Sequence 286848, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 286848  
; LENGTH: 596  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-286848

Query Match 6.1%; Score 204.6; DB 15; Length 596;  
Best Local Similarity 86.9%; Pred. No. 1.7e-44;  
Matches 225; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGTTATCCCTCAATCATCTGGTATCAATATATATATTTTTCACATTC 60  
Db 525 TAAACCAAGAGGTTATCCCTCAATCATCTGGTATCAATATATATATTTTTCACATTC 466  
QY 61 TGTACTTTTTTAATGAGATTGAGGTTGTTCTGTGATTTGTTATCAGAAATPACCAATGCAC 120  
Db 465 TGTACTTTTTTAATGAGATTGAGGTTGTTCTGTGATTTGTTATCAGAAATPACCAATGCAC 406  
QY 121 AAAGCCAGAGTATTTTGGAACTAGAGAGCTATTTTGGTATTTTGGATTTTCTCCA 180  
Db 405 AAAGCCAGAGTATTTTGGAACTAGAGAGCTATTTTGGTATTTTGGATTTTCTCCA 346  
QY 181 AGTTCAAGGAACCAAGAGATATCTCCATTAAACATATACCATCTCGAAACTAAAGACATAGA 240  
Db 345 AGTTCAAGGAACCAAGAGTAAAGTACTTAAATGTTTACTTTTAAATGCTTATCTATAA 286  
QY 241 CAATCCCCCAAGAAATGAA 259  
Db 285 ATCTACCGATAGAAGTAA 267



OTHER INFORMATION: Mouse IPW 200 cDNA sequence (partial)

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(4204)

OTHER INFORMATION: n is a, c, g, or t.

US-10-007-270-23

Query Match 5.9%; Score 197.8; DB 13; Length 4204;

Best Local Similarity 62.8%; Pred. No. 4.7e-42;

Matches 307; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 1877 GTTCTATGACATGGCCCAAGCGGCGAGAGCTGTGGAGTCTCTTTCAGTCTCGGTG 1936

Db 2152 GTGTTCTGAGTCACACCGAGCTGCAGAGCATTTGGTGTCTTTCAGGCTCGGCTGA 2211

QY 1937 CTAACATGGCTCTTCCACAGACTGTTCAACAGAGCTCTCTGGAGTACCGAGCTCTG 1996

Db 2212 CAACATGTTGTTTTCAGAGACTGTTTAAACAAAACCTCTTTGGAATATAAAGCCCTGG 2271

QY 1997 AGCAACAATTACACAGCTGCTGTTCCATATCTACGATCCAATCTTACAGGATTTAAGC 2056

Db 2272 AACAAAGATTCTTAGAAGCTGCTGCTCCCTATCTCCAGTCAAACTCTCAGGCTTCCAG 2331

QY 2057 AACTGGAATACTTAATCTCAGAAACGGAGTGTGATGTGAATAGCAAAATGAAGTTG 2116

Db 2332 ACCTAGAAATCCCTGAGTTTCAGAAACGGCAGCATTTGTGTGAACAGCCGAGTGAGTTG 2391

QY 2117 CTAAGTCTGCGGTATAACTCACCAGGCTGTGCACGGGGCTTGGAGGATTTTCGTT 2176

Db 2392 CCGAGTCTGCCCTCTTAAGTCTACAGGCCATGTATAGGATCTGGAGACTTTTGTGA 2451

QY 2177 CTGCTGAGCCCAACAACTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACCG 2236

Db 2452 CCATGCTCTACCAACCATGAATCTGGATATCGAATAGTACTCCCTGGAGCTGGAATCAG 2511

QY 2237 CTGATCAAGCAGATCCCTGCAAGTCTCTGCTGCGCGGATTTGCCAATGTGAAGA 2296

Db 2512 GTGATGAGCCCAACCCCTTGAAGTTTCAGGCTGTGAATGAATTTCTGAGTGTTCGTA 2571

QY 2297 ACGAACGAGTCTGAGGAGCGGAGTGTGCTGCAACACGAGATATGACAGCCGCGGAGC 2356

Db 2572 ATCCATGAGTGGAGAGCAAGTGCAAAATGCTACCTGGTACCTGAGTGTGGATGAC 2631

QY 2357 TGAACGCTC 2365

Db 2632 TGCCTGTC 2640

## RESULT 13

US-10-007-270-18

Sequence 18, Application US/10007270

Publication No. US20020160954A1

GENERAL INFORMATION:

APPLICANT: Hageman, Gregory S.

APPLICANT: Kuehn, Markus H.

APPLICANT: University of Iowa Research Foundation

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES

FILE REFERENCE: 020618-00012005

CURRENT APPLICATION NUMBER: US/10/007,270

PRIOR FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US 09/430,195

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 09/183,972

PRIOR FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 2964

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human IPW 200 cDNA sequence, isoform C

US-10-007-270-18

Query Match 5.5%; Score 184.8; DB 13; Length 2964;

Best Local Similarity 66.1%; Pred. No. 1.2e-38;

Matches 267; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 1883 TGACCAATGGCCCCAAGGCGGAGAGCTGTGTAGTGTCTTTCAGTCTCGGTGTGCTAACA 1942

Db 2520 TGAGTTATACCAGACTTCAGAGAGCTTTGGTGTCTTTCAGGCTCCGAGTGACTAACA 2579

QY 1943 TGGCCCTCTCCAAAGACCTGTTCACAAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAC 2002

Db 2580 TGATGTTTTCAGAGATCTGTTTAAATAAAACTCTCTGGAGTATAAAGCCCTGGAGCAAA 2639

QY 2003 AATTCCACAGCTGCTGTCTCCATATCTACGATCCAATCTTACAGGATTTTAAGCAACTTG 2062

Db 2640 GATTTTGAATGCTGTCTCCCTATCTCCAGTCAATCTCAGGCTTCAGAACTTAG 2699

QY 2063 AAATATCTTAATCTCAGAAACGGAGTGTGATTTGAAATAGCAAAATGAAGTTTCTAAGT 2122

Db 2700 AAATCCTCAACTTCAGAAATGGCAGCATTTGGTGTGAACAGTCGAATGAAGTTTGCAATT 2759

QY 2123 CTGTGCGGTATATACCTCACCAGGCTGTGCACGGGGTCTTGGAGGATTTTCGTTCTGCTG 2182

Db 2760 CTGTCCCTCCCTTAAGTCAACCAATGCGGTGTACATGATTTCTGGAAGACTTTTGTACCACTG 2819

QY 2183 CAGCCCAACAACCTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACCCAGCTGATC 2242

Db 2820 CCTACAAATACCATGAACCTTGGCTATTGATAAATACTCTCTTGAATGGAATCAGGTGATG 2879

QY 2243 AAGCAGATCCTCGAAGTTCCTGSCCTCGCGCGAATTTTGCCCAA 2286

Db 2880 AAGCAACCTTTCGAAGTTTCAGGCTGTGAATGAATTTTCAGAA 2923

## RESULT 14

US-10-311-455-2147/c

Sequence 2147, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: PIERPENS, Kurt

APPLICANT: BERLIN, Kurt

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 2147

LENGTH: 113515

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-2147

## Query Match

Best Local Similarity 1.8%; Score 61; DB 14; Length 113515;

Matches 193; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

QY 2444 ATCACTCTGAAAAATCAAGCATACAAAACTAGTGTAAAAAGTTCCAAAAATCAACAAAAATA 2503

Db 51718 ATTAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 51659

QY 2504 ACAAGGTAATCAGTAAAGAAATTTCTGAATTTCTGACCGTAGAATATGAAGATTTTAACC 2563

Db 51658 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 51599

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QY 2564 ATCAAGATTGGGAAGGAATTTAAAACTGAAATGTGCAATATATCACTTAGGCTATCTCA 2623
Db 51598 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 51539
QY 2624 AGAGAGAGATTGCTCTCAAGGAAATGGAGACAGGCATATTTCATGGGTCAATCAAAA 2683
Db 51538 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 51479
QY 2684 TCCAGACATACAGTCACACCTGAGAAATCAGCACACACCATATTTCAATATAGAGAGTC 2743
Db 51478 AACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAATACAGCAACAAAATTTACAAAATACACATTT 51419
QY 2744 ATGTACTTTGGCAACAGTAATTTCTGAAAAAAGAGACACTTACTATTATTAAACCCCA 2803
Db 51418 AAATCATTTTCCCCACACAAATAAAAAATAAACTTACCACATTAACTACTACTCTA 51359
QY 2804 AATGCAATCAGCGAAACATATTTTACTATTCTTTGGATGATAGTCAAAATGAT 2856
Db 51358 AAAAAACCAATTAATAAAATCCTTTCTTTATTATATAATTTTAAAAACGAT 51306
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RESULT 15
US-09-908-975-16399
; Sequence 16399, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36588-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16399
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-16399
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Query Match 1.8%; Score 60; DB 10; Length 60;
Best Local Similarity 100.0%; Pred.No. 5.6e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3009 GCAGGAGATGCAGGTCTCTCTTAACCGCATGAATGTATGTAGTGTAGGACCTGTAGTG 3068
Db 1 GCAGGAGATGCAGGTCTCTCTTAACCGCATGAATGTATGTAGTGTAGGACCTGTAGTG 60
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Search completed: March 1, 2004, 20:51:26  
Job time : 1096 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 14:09:16 ; Search time 230 seconds  
(without alignments)  
8034.724 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaaccaagaaggttatctct.....tactatatgacataatcaat 3330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*

2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PCUS COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	57.4	1.7	7218	1	US-08-232-463-14
C 2	44.8	1.3	5562	1	US-10-204-708-63
C 3	44.6	1.3	5852	1	US-07-867-106-2
C 4	43.6	1.3	6243	2	US-09-056-075-1
C 5	43.2	1.3	8607	4	US-10-204-708-72
C 6	43	1.3	1035	4	US-09-134-001C-687
C 7	42.6	1.3	1664976	4	US-08-916-421B-1
C 8	42	1.3	832	4	US-09-621-976-2813
C 9	41.6	1.2	7304	4	US-10-204-708-43
C 10	41.2	1.2	2244	4	US-10-204-708-2
C 11	41.2	1.2	10457	4	US-08-356-171B-270
C 12	40.8	1.2	640681	4	US-09-790-988-1
C 13	40.6	1.2	832	4	US-09-621-976-2813
C 14	40.2	1.2	4970	1	US-08-764-100-14
C 15	40.2	1.2	4970	1	US-08-764-100-20
C 16	40.2	1.2	63588	4	US-09-873-404-3
C 17	40	1.2	6306	4	US-10-204-708-50
C 18	39.8	1.2	580073	4	US-08-545-528D-1
C 19	39.6	1.2	6113	4	US-10-204-708-14
C 20	39.6	1.2	7218	1	US-08-232-463-14
C 21	39.6	1.2	19513	4	US-10-204-708-39
C 22	39.4	1.2	2429	3	US-09-386-493-3
C 23	39.2	1.2	2733	4	US-09-134-000C-1272
C 24	38.8	1.2	5152	4	US-10-204-708-74
C 25	38.8	1.2	8537	4	US-10-204-708-41
C 26	38.6	1.2	1310	4	US-09-721-870-110
C 27	38.6	1.2	5360	4	US-10-204-708-65

C 28	38.2	1.1	16550	4	US-08-916-421B-3
C 29	38.2	1.1	19124	2	US-08-487-826B-13
C 30	38.2	1.1	1664976	4	US-08-916-421B-1
C 31	37.8	1.1	1318	4	US-09-719-108-5
C 32	37.8	1.1	1696	4	US-09-835-811-1
C 33	37.8	1.1	2555	2	US-08-960-022-15
C 34	37.6	1.1	399	4	US-09-621-976-8976
C 35	37.6	1.1	5152	4	US-10-204-708-47
C 36	37.6	1.1	5610	4	US-10-204-708-54
C 37	37.6	1.1	6368	4	US-10-204-708-68
C 38	37.4	1.1	5455	4	US-10-204-708-34
C 39	37.4	1.1	5501	4	US-10-204-708-38
C 40	37.2	1.1	658	3	US-08-998-416-595
C 41	37.2	1.1	2223	1	US-08-257-073-4
C 42	37.2	1.1	6306	4	US-10-204-708-50
C 43	37.2	1.1	43360	4	US-09-453-702B-206
C 44	37.2	1.1	45325	4	US-09-453-702B-261
C 45	37	1.1	505	4	US-09-621-976-15639

#### ALIGNMENTS

#### RESULT 1

US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHREIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)693-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-Fis  
; US-08-232-463-14

Query Match 1.7%; Score 57.4; DB 1; Length 7218;



Best Local Similarity 7.1%; Pred. No. 6.1e-06;  
Matches 31; Conservative 225; Mismatches 181; Indels 0; Gaps 0;

Qy 2227 ATTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCTCGCCTCGCGCGAATTTGCCAA 2286  
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Db 1473 ATCTATGCAAGTAGTTAAAGAGATAGAAGAAATTGGTACRRRRRRRRRRRRRRRR 1414  
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Qy 2287 TGTGTAAGAACGACGAGCTGAGGAAGCGGAGTGTGCTGCAACACGAGATGACAGC 2346  
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Db 1413 RRR 1354  
|||  
Qy 2347 CAGGGGAGCTGCGGCTCTGGAACACGAGCTGTGCGCCTCGCACAAGAGGAATCGAG 2406  
|||  
Db 1353 RRR 1294  
|||  
Qy 2407 GTCTTCAGGAAGGAGCTCCATGAGGTGCGCAGATCACTCTGMAAATCAAGCATAC 2466  
|||  
Db 1293 RRR 1234  
|||  
Qy 2467 AAAACTAGTGTAAAGATTCCAAAGTTCACAAATCAACAAATCAAGGTAAATCAGTAAAGAAAT 2526  
|||  
Db 1233 RRR 1174  
|||  
Qy 2527 TCTGAATCTGACCGTAGAATATGAAGAAATTAACATCAAGATTGGGAGGAATTA 2586  
|||  
Db 1173 RRR 1114  
|||  
Qy 2587 AAACGTGAATGTCAATATCACTTAGGCTATCTCAAGAGATGATTTGCTTCTCAA 2646  
|||  
Db 1113 RRR 1054  
|||

Qy 2647 GGAAATGGAGACGC 2663  
|||  
Db 1053 TCGACCTGCAGCAAGC 1037  
|||

RESULT 2  
US-10-204-708-63/c  
; Sequence 63, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 63  
; LENGTH: 5562  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-63

Query Watch 1.3%; Score 44.8; DB 4; Length 5562;  
Best Local Similarity 44.9%; Pred. No. 0.028;  
Matches 210; Conservative 0; Mismatches 257; Indels 1; Gaps 1;

Qy 2394 AAAGGAATGCGAGTCTCCAGGAAAGGAGTCCATGTCAGGTGCCAGATCACTCTGA 2453

Db 1956 AAATATATACGACGACGAAACAAATACCTAACCAATTAACCACTACCAATPACA 1897  
|||  
Qy 2454 AAATCAAGCATACAAAAGTAGTGTAAAGAGTTCCAAAATCAACAAAATACAAAGGTAAT 2513  
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Db 1896 AAACACATATATCTCTCTTAATCGAAAAAACTACTTCAATATAAAAAATATAACCTAAAA 1837  
|||  
Qy 2514 CAGTAAAGAAATTTCTGNATTACTGACCGTAGAATATGAAGAATTAACCATCAAGATTG 2573  
|||  
Db 1836 CCTAATAAAAAATAAATAATATACCTTCAAAATAAAAAAACTACCATTAATAAAAAAT 1777  
|||  
Qy 2574 GGAAGAAATTAAAAACTGAAAATGTAATATCACTTAGGCTATCTCAAGAGAGATGA 2633  
|||  
Db 1776 CATCATATTTCTCAAAACGAAACGTAATAAATAAATCAATAAAAAACAAAAAAATAA 1717  
|||  
Qy 2634 TTTGCTTCTCAAGGAAATCGACAGGCAATATTCATGGGTATCAATAATCCAGA-CAT 2692  
|||  
Db 1716 AAACCATCATATAAATAAAAAAAACAAAAATAAATAAATAAATAAATATATTATTCAC 1657  
|||  
Qy 2693 ACAGTCAACACTGAGAATCGACACACACCATATTTCAAAATATAGAAGTCTACTTGTG 2752  
|||  
Db 1656 AAATTTCTAAATAAACAATCTCTTAAAAAATAAATAAATAAATAAATAAATAAATAA 1597  
|||  
Qy 2753 GCAACCACTAAATTTCTGAAAAAAGACACTTACTTATTATAAACCCCAATGCAATC 2812  
|||  
Db 1596 TAACTTTCTTAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1537  
|||

Qy 2813 AGCGAAACATATTTTACTATTTCTTGGATGATAGTCAAAATGATCATA 2860  
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Db 1536 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1489  
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RESULT 3  
US-07-867-106-2/c  
; Sequence 2, Application US/07867106  
; Patent No. 5389526  
; GENERAL INFORMATION:  
; APPLICANT: Slade, Martin B  
; APPLICANT: Chang, Andy C M  
; APPLICANT: Williams, Keith L  
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular  
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris  
; STREET: One Liberty Place 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/867,106  
; FILING DATE: 19920625  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PJ 7187  
; APPLICATION NUMBER: PCT/AU90/00530  
; FILING DATE: 02-NOV-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feeney, Joanne Longo  
; REGISTRATION NUMBER: 35,134  
; REFERENCE/DOCKET NUMBER: RICE-0002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5852 base pairs  
; TYPE: NUCLEIC ACID

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2378..5038  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2378..5038  
US-07-867-106-2

Query Match 1.3%; Score 44.6; DB 1; Length 5852;  
Best Local Similarity 51.1%; Pred. No. 0.033;  
Matches 156; Conservative 0; Mismatches 144; Indels 7; Gaps 2;

QY 42 TAATATTTTTCACATTCGTTACTTTTAAAGAGATTGAGTTGTTCTGTGATGTT 101  
Db 2065 TAATTAATATTATAATGAGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTCAAGTA 2006  
QY 102 ATCAGAAATACCAATGCACAAAAGCCAGAAATGTTTGGAACTAGAAGAGCTATTTTG 161  
Db 2005 AAAAAAAGAAAAAAGAG-----AATAGAAAAAGTTGTTTAACTACATTAG 1951  
QY 162 TTTTGGATTTTTCAGATTCAAGAACCAAGATATCTCCATTAACATATACCAT 221  
Db 1950 TTTTATATGTTTTCATATTATAAATAAATCTTTTAAATTTTAAATGATTTTAA -ATT 1893  
QY 222 CTGAATAAGACATAGACAAATCCCAAGAAATGAAACAACTGAAAGTCTGAAAAA 281  
Db 1892 ATGAGATCTAATAAATAAATAAATTTTAAATTTAAATAAAGAAAAAAGAAAAA 1833  
QY 282 TGTACAAATGTCACATGAGACGAATATTCGATTGGCAAGCATCGAACAAAAAGAT 341  
Db 1832 AGTAGAATTTAATAAATAAATAAATTTTCAATCTTAATAATTAAGTATATATCGAT 1773  
QY 342 CGCATTTT 350  
Db 1772 AGCAATTT 1764

RESULT 4  
US-09-056-075-1  
; Sequence 1, Application US/09056075  
; Patent No. 595368  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Eric A.  
; APPLICANT: Bradshaw, Marite  
; APPLICANT: Rood, Julian  
; TITLE OF INVENTION: Expression System for Clostridium  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,075  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27386  
; REFERENCE/DOCKET NUMBER: 960296.95238  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6243 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 3770..4013  
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from  
; OTHER INFORMATION: plasmid RP4"  
US-09-056-075-1

Query Match 1.3%; Score 43.6; DB 2; Length 6243;  
Best Local Similarity 55.2%; Pred. No. 0.069;  
Matches 85; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 2453 AARATCAGCATACAAACTAGTCTTAAAAAGTTCCAAATCAACAAATCAACAGGTAA 2512  
Db 1229 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 1288  
QY 2513 TCAGTAAAGAAATTCGAATTACTGACCGTAGAATATGAAGATTTTAAACCATCAAGATT 2572  
Db 1289 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 1348  
QY 2573 GGAAGAAATTAATAACTGAAATGTACAAATTA 2606  
Db 1349 TATAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 1382

RESULT 5  
US-10-204-708-72/c  
; Sequence 72, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; PRIOR FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 72  
; LENGTH: 8607  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-72

Query Match 1.3%; Score 43.2; DB 4; Length 8607;  
Best Local Similarity 50.4%; Pred. No. 0.11;  
Matches 131; Conservative 0; Mismatches 128; Indels 1; Gaps 1;  
QY 2454 AATCAGCATACAAACTAGTGTAAAAAGTTCAAAATCAACAAATCAACAGGTAA 2513  
Db 7055 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 6996



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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g

; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1

Query Match
Best Local Similarity 1.3%; Score 42.6; DB 4; Length 1664976;
Matches 162; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 2928 TTATTGTTTAGGGAAGTGAACAATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTAC 2987
Db 710981 TTATTTCCATGGTATTCACATTTAGATTATTGCTAACTTCATCAACATTAAACTATA 710922

QY 2988 ATTAAAGATGACTACTTACGAGGAGAGATGCGAGGTCTCTCTAAAGCGCATGAATGATG 3047
Db 710921 ACATAACCAATGACAAACAAACGGAACAAATGGGTAGGTTTTTATAACATTAGTTGTCA 710862

QY 3048 TAGTGCTAGGCACTGTAGTGAGTGATATATGCTCCACACTACTGCTGATAAACACAAA 3107
Db 710861 GGGATTTTCCCTCCATATAGAGTTTTTTATTTTTCGATGTCCTCATTTGGATAACCT 710802

QY 3108 CCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGCTTACATAGPAGA 3167
Db 710801 TCTCCATCGGTAAATATATTTCTTTTTCATTTTCTTTGATTTTCATGTTCTTAATAGAAAT 710742

QY 3168 CTGTTTGTGGCAATAATCTTTGAAATGTTCTTTAAAGAACTGAGGTTTCAGATACAC 3227
Db 710741 TTATCTTTTCATTTATTTAAAGTTTCTTCTCAACCCATCTTTGCTATTATTATA 710682

QY 3228 ATACCATGGAAAAATCTACTTTTCTTTGTTTACTACAAAGCTATTTTAAAGAGATGCT 3287
Db 710681 ACATCCCTCAAAATATCTCCTTCTTTTAAATCTTTCAATATGTTTTTTGTCAGAGTTTCT 710622

QY 3288 A 3288
Db 710621 A 710621

RESULT 8
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
```



```
;
;
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-08-956-171E-270

Query Match
Best Local Similarity 1.2%; Score 41.2; DB 4; Length 2244;
Matches 82; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 2447 ACTCTGAAATCAAGCATACAAAACAGTCTTAAAGATTCCAAATCAACAAATAACA 2506
Db 518 ATTATATAATAGTCAATGCGACCAAGTTTATTATGATGGATTATATAAAGAACA 577

QY 2507 AGGTAATCAGTAAAGAAATCTGAATCTAGCCGTAGAAATGAGAAATTTAACCATC 2566
Db 578 AGTAAACGAAACAAAGAAATTTTGTGTTTTTAATACGTGAATATAAGATTATTGATATA 637

QY 2567 AAGATTCGGAGGAATTTAAAACTGAAA 2596
Db 638 AAGTTTTCAAAGTTATACAAAAGATAA 667

RESULT 11
US-10-204-708-2/c
; Sequence 2, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-2

Query Match
Best Local Similarity 1.2%; Score 41.2; DB 4; Length 10467;
Matches 186; Conservative 0; Mismatches 223; Indels 1; Gaps 1;

QY 2447 ACTCTGAAATCAAGCATACAAAACAGTCTTAAAGATTCCAAATCAACAAATAACA 2506
Db 8253 ACTAATAAAATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8194

QY 2507 AGGTAATCAGTAAAGAAATCTGAATCTAGCCGTAGAAATGAGAAATTTAACCATC 2566
Db 8193 AAAAACAACGTAAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8134

QY 2567 AAGATTCGGAGGAATTTAAAACTGAAAATGATGATGATGATGATGATGATGATG 2626
Db 8133 TATTTCGATTAATCGCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8075

QY 2627 GAGATGATTTGCTTCTCAAGGAATGAGCAGCATATTCATGGGTCATCAAAATCC 2686
Db 8074 CAAATATTTTAAATTTATTCAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8015
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QY 2687 AGACATACAGTCAACACTGAGAATCAGCACACACCATATTTTCAATATAGAGAGTCATG 2746
Db 8014 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 7955

QY 2747 TACTTGGCAACAGTAATCTGAAAAAAGACACACTTACTTATTTAAACCCCAAT 2806
Db 7954 ATAAATATAACTAATAATACTAAACGATAAAAAAACTTTTAATATAAAAAACACTAAA 7895

QY 2807 GCATTCACGCGAAACATATTTTACTATTTCTTGGATGATAGTCAAAATCAT 2856
Db 7894 TTCTCCAAAAAATAAACAATTTAAATAATATAAAAAACACTTAATAAT 7845
```

```
RESULT 12
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
```

```
Query Match
Best Local Similarity 1.2%; Score 40.8; DB 4; Length 640681;
Matches 130; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

QY 45 TTATTTTTCACATTTCTGTTACTTTTAAATGAGATTTGAGTCTCTGTGATTTTATC 104
Db 297756 TCTTTTCTCTTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 297815

QY 105 AGAATTACCAATGCACAAAAGCCAGAAATGTATTTGGAACTAGAAAGAGCTATTTTGT 164
Db 297816 AGAATTTCTAAGAACATTTCTCGTGAATGTACACGAAGTGTACGAATATTATTAGA 297875

QY 165 TTTGATTTTCTCCAAAGTTCAAGAACCAAGATATCTCCATTAACATATACCATTTCTG 224
Db 297876 TTTAGTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 297932

QY 225 AAATTAAGACATAGACAAATCTCCCAAGAAATGAAACAACTGAAAGTACTGAAAAATGT 284
Db 297933 TTACTTAAATTAATATCAAAATGAGAAATTAATTAATTTTAAATATTTTAAAGACT 297992

QY 285 ACAAATGTCACTATGAGA 304
Db 297993 GATTATTAAACATATAAAA 298012
```

```
RESULT 13
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
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; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match
Best Local Similarity 12.5%; Score 40.6; DB 4; Length 832;
Matches 47; Conservative 176; Mismatches 150; Indels 2; Gaps 2;

QY 2920 TAGCTTACTTATTTAGGACCTGGAACAATTTATGGGAAGCAACTCTTTATATGCTA 2979
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5 WNKYTTWYAKWTWKWSWSYMYMKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKY 64
QY 2980 GAAAGTACATTTAAAGATGACTACTTACGCGAGGATCGAGTCTCTCTAAACGCA-T 3038
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 WGTYKKAMCRKTKKKKKYGMWMTWGWRSVMAMWTRTWGYAYRSMYKWTWRYRCW 124
QY 3039 GAATGTATGTAGTGTAGGACCTGTAGTGTAGTGTATATGTCTCCACACTACGCTGTAT 3098
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 KKYAYRKTTCTSSKGTWTKWKKAWTTWKKYVYAAATRYMMCMWTKRWASWYVC 184
QY 3099 AAACACAACTCAGTATTC-A-GTTATTAGGCACACTAGTTTATACGCAACTACTGCTT 3157
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 WNWGKARKSTWRKRSYASARSAXRCCSCSGWMSKTYMWRWNRWNRWNRWNRWNRW 244
QY 3158 ACATAGTAGACTGTTTGTGTCCTCAATATCTTTGAATGTCTTTAAAGAAACTGAGGT 3217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
245 ASCNMRKRYAGKSTSYKSMWYCWTRSKYCYTKARWTGYCYRKGGMWGRGRWYASK 304
QY 3218 TCAGATACATACCATGGGAAAATCTACTTCTTCTGTACTACACAAAGCTATTTTAA 3277
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
305 YMKRWCMWCMARMYRYSTGTASWRRRYTWMKWKYAWARAARWMMWMMWAWERAC 364
QY 3278 AGAAGATGCTATGTT 3292
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
365 AAAATAATAATTTT 379

RESULT 14
US-08-764-100-14
; Sequence 14, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gielen L., Johannes J.
; APPLICANT: Peters, Dirk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,100
; FILING DATE: 06-DEC-1996
```

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,064
; FILING DATE:
; APPLICATION NUMBER: US 08/032,235
; FILING DATE: 17-MAR-1993
; APPLICATION NUMBER: GB 9206016.9
; FILING DATE: 19-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5773700r18, Allen E.
; REGISTRATION NUMBER: 34,490
; REFERENCE/DOCKET NUMBER: 137-1061
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 354-3592
; TELEFAX: (415) 857-1125
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-764-100-14

Query Match
Best Local Similarity 1.2%; Score 40.2; DB 1; Length 4970;
Matches 155; Conservative 0; Mismatches 173; Indels 1; Gaps 1;

QY 23 ATCTCTCGTATCAATATATATTTTTCACATTTCTGTACTTTTATGAGATTG 82
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
976 ATCAITTGATATGAATCTAAATATGTTTCATTTAATAATAATATATATATTTGTC 1035
QY 83 AGGTTGTTCTGTGATGTATCAGAAATACCAATGCGACAAAGCCAGATGTATTGGAA 142
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1036 ATAATATTTTG-AATGTTTAAAGTAAAAATAAGCAAGATAAAAACTATATATATAT 1094
QY 143 ACTAGAAGAGCTATTTTGTGTTTGTGTTTCTCCAAGTTCAAGGAACCAAGATATC 202
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1095 ATATATGAAGATTAATAATATATATGTTTGTGTTTAAACAAATCAAAACCAAAA 1154
QY 203 TCCATTACATATACCATCTTGAAACTTAAGACATAGACATATCCCAAGAAATGAAACA 262
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1155 AGAAAAAGAAAAAATAAACAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAA 1214
QY 263 ACTGNAAGTCTGAAAAATGTACAAATGTCAAAATGTCACTATGAGACGAATATTCGATTGCA 322
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1215 AATGAAAAAGTTGAAAAAACCAAAAAACCAAAAAAATTTTTTGTAAATAATAAGGCTCCGGC 1274
QY 323 AAGCATCGAACAAAAAGATCCGCTTTT 351
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1275 CAGATTGCTCTAAGACCTTTTATTGTT 1303

RESULT 15
US-08-764-100-20/c
; Sequence 20, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gielen L., Johannes J.
; APPLICANT: Peters, Dirk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
```

Search completed: March 1, 2004, 20:33:06  
Job time : 241 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 12:39:46 ; Search time 1245 Seconds  
(without alignments)  
11362.650 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaacaaagaagttatctct.....tactatatgacataatcaat 3330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373963 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002s:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3330	100.0	3330	7	ADAL4840 Human int
2	3330	100.0	3330	8	ACC57946 Human int
3	3125.6	93.9	3263	3	AAA46205 CDNA enco
4	3124.6	93.8	3261	7	ADAL4866 Human cdn
5	3124.6	93.8	3261	8	ACC57960 Human int
6	2765.8	83.1	2887	7	ADAL4842 Human int
7	2765.8	83.1	2887	8	ACC57947 Human int
8	2724.6	81.8	2966	3	AAA46328 Interphot
9	2184.2	65.6	2244	3	AAA46329 Interphot
10	2184.2	65.6	2244	7	ADAL4844 Human int
11	2184.2	65.6	2244	8	ACC57948 Human int
12	1375.6	41.3	3668	7	ADAL4847 Mouse int
13	1375.6	41.3	3668	8	ACC57950 Mouse int
14	1127.2	33.8	3206	3	AAA46309 CDNA enco
15	534	16.0	1726	7	ADAL4849 Mouse int
16	534	16.0	1726	8	ACC57951 Mouse int
17	491.6	14.8	1321	7	ADAL4851 Mouse int
18	491.6	14.8	1321	8	ACC57952 Mouse int
19	439	13.2	555	3	AAA46204 CDNA enco
20	439	13.2	555	7	ADAL4853 Monkey in
21	439	13.2	555	8	ACC57953 Monkey in
22	204.6	6.1	1858	3	AAA46327 Exon 1 an
23	204.6	6.1	1858	7	ADAL4846 Human int

24	204.6	6.1	1858	8	ACC57949 Human int
25	203.4	6.1	4165	3	AAA46206 CDNA enco
26	203.4	6.1	4166	7	ADAL4855 Human int
27	203.4	6.1	4166	8	ACC57954 Human int
28	197.8	5.9	4204	3	AAA46310 CDNA enco
29	197.8	5.9	4204	7	ADAL4862 Mouse int
30	197.8	5.9	4204	8	ACC57958 Mouse int
31	184.8	5.5	2964	7	ADAL4857 Human int
32	184.8	5.5	2964	8	ACC57955 Human int
33	103	3.1	1094	3	AAA46321 Exon 13 o
34	61.8	1.9	1088	3	AAA46312 Exon 3 of
c	61	1.8	113515	6	ABL34174 Human imm
35	60	1.8	60	6	ABL34174 Human imm
36	57.6	1.7	1817	3	AAA46320 Exon 12 o
37	57.6	1.7	1817	3	AAA46320 Exon 12 o
38	56.4	1.7	434	5	ABV58531 Human pro
c	54.6	1.6	3683	7	ABZ10199 Haematopo
c	54	1.6	16633	6	ABN79984 Human che
c	41	1.6	6255	6	ABL32960 Human imm
c	42	1.6	516	7	ABX40620 Bovine ES
c	43	1.6	6775	6	ABQ67159 Human ang
c	44	1.6	2000	7	ADA71938 Rice gene
c	45	1.6	5586	6	ABK40004 Human che

#### ALIGNMENTS

RESULT 1

ADAL4840

ID ADAL4840 standard; cdna; 3330 BP.

XX AC ADAL4840;

XX DT 06-NOV-2003 (first entry)

XX DE Human interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.

XX KW ss; gene; human; IPMC 150 isoform A; gene therapy;

XX KW interphotoreceptor matrix component; IPMC; ocular disorder;

XX KW macular degeneration; photoreceptor death; retinal detachment.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT CDS 131..2586

FT FT /\*tag= b

FT FT /product= "IPMC 150 isoform A"

FT FT /transl\_except= (pos:689..756,aa:Thr-Asp)

FT FT sig\_peptide 131..190

FT FT /\*tag= a

FT FT /label= Signal\_sequence

FT FT mat\_peptide 191..2583

FT FT /\*tag= c

FT FT /label= Mature\_IPMC\_150\_isoform\_A

FT FT misc\_feature 692..753

FT FT /\*tag= d

FT FT /note= "This region could represent intronic sequence not removed from the cDNA sequence"

FT FT

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FT FT

DR P-PSDB; ADA14841.  
XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX  
XX  
PS Claim 3; Page 29-30; 76pp; English.  
XX  
CC The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding human  
CC interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX  
SQ Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 3330; DB 7; Length 3330;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TAAACCAAGAGGTATCTCTCAATCATCTGGTATCATATAATTAATTTTTCACATTTTC 60  
DB 1 TAAACCAAGAGGTATCTCTCAATCATCTGGTATCATATAATTAATTTTTCACATTTTC 60  
  
QY 61 TGTACTTTTAAATGAGATTGAGTTGTTCTCTGATGTTATCAGAAATACCAATGAC 120  
DB 61 TGTACTTTTAAATGAGATTGAGTTGTTCTCTGATGTTATCAGAAATACCAATGAC 120  
  
QY 121 AAAAGCCAGATGTAATGGAACACTAGAGAGCTATTTTGTGTTTTCGATTTTCTCCA 180  
DB 121 AAAAGCCAGATGTAATGGAACACTAGAGAGCTATTTTGTGTTTTCGATTTTCTCCA 180  
  
QY 181 AGTTCAAGGAACCAAGAGATATCTCCATTAACATATACCATCTGAAACTTAAAGACATAGA 240  
DB 181 AGTTCAAGGAACCAAGAGATATCTCCATTAACATATACCATCTGAAACTTAAAGACATAGA 240  
  
QY 241 CAATCCCCCAAGAAATGAAACAACTGAAGTACTGAAATAATGTACAAATGTCAACTAT 300  
DB 241 CAATCCCCCAAGAAATGAAACAACTGAAGTACTGAAATAATGTACAAATGTCAACTAT 300  
  
QY 301 GAGACGAATATTCGATTTGGCAAGCATCGAACAAAGATCGCATTTTCCCAACGGG 360  
DB 301 GAGACGAATATTCGATTTGGCAAGCATCGAACAAAGATCGCATTTTCCCAACGGG 360  
  
QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTA 420  
DB 361 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTA 420  
  
QY 421 TAGATTCAGAGTGTCTCAGAACAGTATGGGAGCATATCGATCTTTCTGGATCGCAT 480  
DB 421 TAGATTCAGAGTGTCTCAGAACAGTATGGGAGCATATCGATCTTTCTGGATCGCAT 480  
  
QY 481 CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCGACGAGAGACCTTCTGCCT 540  
DB 481 CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCGACGAGAGACCTTCTGCCT 540  
  
QY 541 CTTTGGACATTTGGAATAAATTCAGCAATTTCCAGGAGCACCCTGGATCTTCTCAGCAGAG 600  
DB 541 CTTTGGACATTTGGAATAAATTCAGCAATTTCCAGGAGCACCCTGGATCTTCTCAGCAGAG 600  
  
QY 601 AATAAAACAGAGAAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGAAGACATTTGGG 660  
DB 601 AATAAAACAGAGAAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGAAGACATTTGGG 660  
  
QY 661 AGAGCCTGGTGAACCAATTTCTATTTCAACAGCAATCTTACATTTCAAGACTTTGGGCAGT 720  
DB 661 AGAGCCTGGTGAACCAATTTCTATTTCAACAGCAATCTTCTGACACTCTGAGGTTACAGAGCTC 1800

QY 721 ATTCTAAGAAAACCCCTCAGAAGAGCAAAATTCAGATGTTGCCAACGTTCTCACTTGGGCCT 780  
DB 721 ATTCTAAGAAAACCCCTCAGAAGAGCAAAATTCAGATGTTGCCAACGTTCTCACTTGGGCCT 780  
  
QY 781 TTCCCTCTCACTCTGATGACACCCCTCCTCAATGAAATTTCTCGATAATACACTCAACGAC 840  
DB 781 TTCCCTCTCACTCTGATGACACCCCTCCTCAATGAAATTTCTCGATAATACACTCAACGAC 840  
  
QY 841 ACCAAGATGCTCAACACAGAAAAGAAACAGAAATTCGCTGTTGGAGGAGCAGAGGTG 900  
DB 841 ACCAAGATGCTCAACACAGAAAAGAAACAGAAATTCGCTGTTGGAGGAGCAGAGGTG 900  
  
QY 901 GAGTCAGCTCTCTCTGTTAAACCAAGTTCNAGGACAGCTCGTGTACTCCAGTCC 960  
DB 901 GAGTCAGCTCTCTCTGTTAAACCAAGTTCNAGGACAGCTCGTGTACTCCAGTCC 960  
  
QY 961 CCATATTACCAAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAAGATATTAAAGAA 1020  
DB 961 CCATATTACCAAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAAGATATTAAAGAA 1020  
  
QY 1021 CTTCCAGATTCAAAAAATCCATGTTTAGGATTTAGACCAAAAGAAAGAAAGATGGC 1080  
DB 1021 CTTCCAGATTCAAAAAATCCATGTTTAGGATTTAGACCAAAAGAAAGAAAGATGGC 1080  
  
QY 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAA 1140  
DB 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAA 1140  
  
QY 1141 AGCCTCGAAGTACCTCTCTGTTTGAATTCACAAAAATTTGAAAGTGAAGAGTCTAT 1200  
DB 1141 AGCCTCGAAGTACCTCTCTGTTTGAATTCACAAAAATTTGAAAGTGAAGAGTCTAT 1200  
  
QY 1201 CATCGAACCTGGAGGAGGACAGCACCAAGATCTATCTCAGCTACAGACCTCAAA 1260  
DB 1201 CATCGAACCTGGAGGAGGACAGCACCAAGATCTATCTCAGCTACAGACCTCAAA 1260  
  
QY 1261 AGGTGATCAGCAAGCACTAGAGGAGAAACAATCTTTGGATGTGGGACAATTCAGTTTC 1320  
DB 1261 AGGTGATCAGCAAGCACTAGAGGAGAAACAATCTTTGGATGTGGGACAATTCAGTTTC 1320  
  
QY 1321 ACTGATGAATTCGTGATCACTGCCAGCCTTTGGTCTCAGACCCCAATCAGAGCTGCC 1380  
DB 1321 ACTGATGAATTCGTGATCACTGCCAGCCTTTGGTCTCAGACCCCAATCAGAGCTGCC 1380  
  
QY 1381 ACATCTTTTGTGTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTGTTGAA 1440  
DB 1381 ACATCTTTTGTGTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTGTTGAA 1440  
  
QY 1441 CCCAGCTTGAGACAGTGGACGAGAGAGCATGGTCTACCTGACACTTCTGGTCTCCA 1500  
DB 1441 CCCAGCTTGAGACAGTGGACGAGAGAGCATGGTCTACCTGACACTTCTGGTCTCCA 1500  
  
QY 1501 CCTGCTATGGCTCTACCTCCCTGTCAGAGAGCTCCACCTTTCTTTATGGCATCAAGCATC 1560  
DB 1501 CCTGCTATGGCTCTACCTCCCTGTCAGAGAGCTCCACCTTTCTTTATGGCATCAAGCATC 1560  
  
QY 1561 TTCTCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCAAGAAATGCTAGTA 1620  
DB 1561 TTCTCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCAAGAAATGCTAGTA 1620  
  
QY 1621 CCAGGCTCCACCTCCCAACAGTATTTCTGCAATCAGCCAACTGGCTCTGGGAAT 1680  
DB 1621 CCAGGCTCCACCTCCCAACAGTATTTCTGCAATCAGCCAACTGGCTCTGGGAAT 1680  
  
QY 1681 TCACATCCACTGATCTTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTC 1740  
DB 1681 TCACATCCACTGATCTTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTC 1740  
  
QY 1741 AGACACCTAGATGAATGGATCTGTCTGACACTCTGCGCCCATCTGAGGTACAGAGCTC 1800  
DB 1741 AGACACCTAGATGAATGGATCTGTCTGACACTCTGCGCCCATCTGAGGTACAGAGCTC 1800

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QY 1801 AGCGAATATGTTTCTGTCCTCCGATCATTTCTTGGAGGATACCACTCCTGTCTCAGCTTTA 1860
Db 1801 AGCGAATATGTTTCTGTCCTCCGATCATTTCTTGGAGGATACCACTCCTGTCTCAGCTTTA 1860
QY 1861 CAGTATATCACCACATAGTTCTATGACCACTTGCCCCCAAGGCGCAGAGCTGCTAGTGTTC 1920
Db 1861 CAGTATATCACCACATAGTTCTATGACCACTTGCCCCCAAGGCGCAGAGCTGCTAGTGTTC 1920
QY 1921 TTCAGTCTGCGGTGTTCTAAAGTGTCTTCCAGACCTTCTCCAGACCTGTTTCAACAAGAGCTCTCTG 1980
Db 1921 TTCAGTCTGCGGTGTTCTAAAGTGTCTTCCAGACCTTCTCCAGACCTGTTTCAACAAGAGCTCTCTG 1980
QY 1981 GAGTACCGAGCTCTCGAGCAACAATTCACAGCTGCTGCTGCTCCATATCTACGATCCAAAT 2040
Db 1981 GAGTACCGAGCTCTCGAGCAACAATTCACAGCTGCTGCTGCTCCATATCTACGATCCAAAT 2040
QY 2041 CTTACAGATTTAAGCAACTTGAATACTTAACCTTCAGAAACGGGAGTGTGATGTGAAT 2100
Db 2041 CTTACAGATTTAAGCAACTTGAATACTTAACCTTCAGAAACGGGAGTGTGATGTGAAT 2100
QY 2101 AGCAAAATGAAGTTTGTCTGCTGCGGATGCTGCGGTATACCTCACCAGGCTGTGCAGGGGTC 2160
Db 2101 AGCAAAATGAAGTTTGTCTGCTGCGGATGCTGCGGTATACCTCACCAGGCTGTGCAGGGGTC 2160
QY 2161 TTGGAGATTTTGTCTGCTGCGGATGCTGCGGTATACCTCACCAGGCTGTGCAGGGGTC 2220
Db 2161 TTGGAGATTTTGTCTGCTGCGGATGCTGCGGTATACCTCACCAGGCTGTGCAGGGGTC 2220
QY 2221 CTCACATTTGAACAGCTGATCAGCAGATCCCTGCAAGTTTCTTGGGCTGCGGCAATTT 2280
Db 2221 CTCACATTTGAACAGCTGATCAGCAGATCCCTGCAAGTTTCTTGGGCTGCGGCAATTT 2280
QY 2281 GCCCAATGTGAAGAACGAAACGGAGCTGAGGAGCGGAGTGTGCTGCAACACAGGATAT 2340
Db 2281 GCCCAATGTGAAGAACGAAACGGAGCTGAGGAGCGGAGTGTGCTGCAACACAGGATAT 2340
QY 2341 GACAGCCAGGGAGCCTGGAGCGTGTGGAACAGGCTCTGTGGCCCTGTGGCCCTGGCAAGGAA 2400
Db 2341 GACAGCCAGGGAGCCTGGAGCGTGTGGAACAGGCTCTGTGGCCCTGTGGCCCTGGCAAGGAA 2400
QY 2401 TGGAGGTCTTCCAGGAAAGGAGCTCCATGCAAGTTTGCAGATCACTCTGAAATCAA 2460
Db 2401 TGGAGGTCTTCCAGGAAAGGAGCTCCATGCAAGTTTGCAGATCACTCTGAAATCAA 2460
QY 2461 GCATACAAATCTAGTGTGTAAAGTGTCCAAATCAACAAATACAAAGTAAATCAGTAAA 2520
Db 2461 GCATACAAATCTAGTGTGTAAAGTGTCCAAATCAACAAATACAAAGTAAATCAGTAAA 2520
QY 2521 AGAAATCTGAATTTACTGACCGTGAATATGAAGAATTTAACCATCAAGATTGGGAAGGA 2580
Db 2521 AGAAATCTGAATTTACTGACCGTGAATATGAAGAATTTAACCATCAAGATTGGGAAGGA 2580
QY 2581 AATTAAATCTGAAATGTCAATTTACCTTAGCTATCTCAGAGAGATGATTTGCTT 2640
Db 2581 AATTAAATCTGAAATGTCAATTTACCTTAGCTATCTCAGAGAGATGATTTGCTT 2640
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QY 2701 CACTGAGAAATCAGACACACATATTTCAATATAGAGAGTCTATCTTGGCAACCCAG 2760
Db 2701 CACTGAGAAATCAGACACACATATTTCAATATAGAGAGTCTATCTTGGCAACCCAG 2760
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Db 2761 TAAATCTGAAAAAAGACACTTTACTTATTATTAACCCCAATGCAATCAGCGAAAC 2820
QY 2821 ATATTTTACTATTTCTTGGATGATGATCAAAATGATCAAGCAGGTTTGTCTCCACCT 2880
Db 2821 ATATTTTACTATTTCTTGGATGATGATCAAAATGATCAAGCAGGTTTGTCTCCACCT 2880
QY 2881 TCCCTGAAAAATTTTACTCAGAGATCATTTGCAACAGCATAGCTTACTTATTGTTAGG 2940
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## RESULT 2

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ACC57946
ID ACC57946 standard; cDNA; 3330 BP.
XX ACC57946;
XX AC
XX DT
XX 11-AUG-2003 (first entry)
XX Human interphotoreceptor matrix IPM 150, isoform A, cDNA.
DE Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX receptor; ophthalmological; gene therapy; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 131..2586
XX FT /*tag= a
XX FT /product= "IPM 150"
XX FT /transl_except= (pos:668..756,aa:Thr-Asp)
XX sig_peptide 131..150
XX FT /*tag= b
XX FN WO2003039346-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036090.
XX PR 08-NOV-2001; 2001US-00077270.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Hageman GS, Kuehn MH;
XX DR WPI: 2003-441440/41.
XX P-PSDB; ABR42342.
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
PT
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QY 1801 AGCGAATATGTTCTCTGTCAGATCAATTTCTTGGAGGATACCACTCTCTCTCAGCTTTA 1860
Db 1801 AGCGAATATGTTCTCTGTCAGATCAATTTCTTGGAGGATACCACTCTCTCTCAGCTTTA 1860
QY 1861 CAGTATATCACCACTAGTCTATGACCAATGCCCCCAAGGCCGAGAGCTGTAGTGTTC 1920
Db 1861 CAGTATATCACCACTAGTCTATGACCAATGCCCCCAAGGCCGAGAGCTGTAGTGTTC 1920
QY 1921 TTCAAGTCTGGTGTCTCTAAGCTTCTCAAGAGCTCTCTCAAGAGCTCTCTG 1980
Db 1921 TTCAAGTCTGGTGTCTCTAAGCTTCTCAAGAGCTCTCTCAAGAGCTCTCTG 1980
QY 1981 GAGTACCGAGCTCTGAGCAACAATTCACACAGCTCTGTTCCATATCTACGATCCCAAT 2040
Db 1981 GAGTACCGAGCTCTGAGCAACAATTCACACAGCTCTGTTCCATATCTACGATCCCAAT 2040
QY 2041 CTTACAGGATTTAAGCAACTTGAATACCTTAACTTCAAGAGCTGTGATTTGTAAT 2100
Db 2041 CTTACAGGATTTAAGCAACTTGAATACCTTAACTTCAAGAGCTGTGATTTGTAAT 2100
QY 2101 AGCAAAATGAAGTTTGTAAAGTCTGTGCGGTATTAACCTCACCAAGCTGTGCACGGGCTC 2160
Db 2101 AGCAAAATGAAGTTTGTAAAGTCTGTGCGGTATTAACCTCACCAAGCTGTGCACGGGCTC 2160
QY 2161 TTGGAGGATTTTGGTCTGCTCAGCCCAACAACCTTCCATCTGGAATATGACAGCTACTCT 2220
Db 2161 TTGGAGGATTTTGGTCTGCTCAGCCCAACAACCTTCCATCTGGAATATGACAGCTACTCT 2220
QY 2221 CTCACATTTGAACCAAGCTGTATCAAGCAGATCCCTCAAGTTCTTGGCTGGCGGAATTT 2280
Db 2221 CTCACATTTGAACCAAGCTGTATCAAGCAGATCCCTCAAGTTCTTGGCTGGCGGAATTT 2280
QY 2281 GCCCAATGTGTAAGAAAGCGGAGTCTGAGGAGCGGAGTGTGCTGCAAAACCAAGGATAT 2340
Db 2281 GCCCAATGTGTAAGAAAGCGGAGTCTGAGGAGCGGAGTGTGCTGCAAAACCAAGGATAT 2340
QY 2341 GACAGCCAGGGAGCTGAGCGGCTGGAACAGGCTCTGTCGCGCTGGCCCTGGCACAAAGAA 2400
Db 2341 GACAGCCAGGGAGCTGAGCGGCTGGAACAGGCTCTGTCGCGCTGGCCCTGGCACAAAGAA 2400
QY 2401 TGGAGGCTCTCCAGGAAAGGAGCTCCATGCGAGTTGCCAGATCACTCTGAAATCAAA 2460
Db 2401 TGGAGGCTCTCCAGGAAAGGAGCTCCATGCGAGTTGCCAGATCACTCTGAAATCAAA 2460
QY 2461 GCATACAAACTAGTGTAAAGTCTCAAAATCAACAAATATCAAGAGTAAATCAGTAA 2520
Db 2461 GCATACAAACTAGTGTAAAGTCTCAAAATCAACAAATATCAAGAGTAAATCAGTAA 2520
QY 2521 AGAAATCTGAATTAAGCTGAGTATCAAGAAATTTAACCATCAAGATTGGGAGGA 2580
Db 2521 AGAAATCTGAATTAAGCTGAGTATCAAGAAATTTAACCATCAAGATTGGGAGGA 2580
QY 2581 AATTAAAACTGAAATGTACAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCCT 2640
Db 2581 AATTAAAACTGAAATGTACAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCCT 2640
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Db 2641 TCTCAAGAAATGGAGACAGCATATTCATGGGTCTCAAAATCCAGACATACAGTCAA 2700
QY 2701 CACTGAGAAATCAGACACACCATATTTCAAATATGAGAGTCTATGTTGGCAACCCAG 2760
Db 2701 CACTGAGAAATCAGACACACCATATTTCAAATATGAGAGTCTATGTTGGCAACCCAG 2760
QY 2761 TAAATCTGAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAAC 2820
Db 2761 TAAATCTGAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAAC 2820
QY 2821 ATATTTTACTATTTCTTGGATGATGATCAAAATGATCATTAAGCCAGGTTTGTTCACCT 2880
Db 2821 ATATTTTACTATTTCTTGGATGATGATCAAAATGATCATTAAGCCAGGTTTGTTCACCT 2880
QY 2881 TCCCTGAAATTTTACTCAGATCAATTTGCAACAGCATAGCTTACTTATTTAGGG 2940
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Db 2881 TCCCTGAAATTTTACTCAGATCAATTTGCAACAGCATAGCTTACTTATTTAGGG 2940
QY 2941 ACTGAACAATTTTATTTGGAAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000
Db 2941 ACTGAACAATTTTATTTGGAAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000
QY 3001 CTACTTACGAGGAGGAGTGCAGGTCTCTCTAAACCGCATGAATGTATGTAGTGTAGGCA 3060
Db 3001 CTACTTACGAGGAGGAGTGCAGGTCTCTCTAAACCGCATGAATGTATGTAGTGTAGGCA 3060
QY 3061 CTGTAGTACGAGTATATATGCTCCACACTACGCTCTGATAAACCAACACCTCAGTATTCAG 3120
Db 3061 CTGTAGTACGAGTATATATGCTCCACACTACGCTCTGATAAACCAACACCTCAGTATTCAG 3120
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Db 3121 TTATTAGGCACTAGTCTTATACGCAACTCTCTTACATAGTACAGTCTTTTGTGGC 3180
QY 3181 AATAATCTTTGAATTTCTTTTAAAGAACTGAGGTTTCAATACATACCATGGAATA 3240
Db 3181 AATAATCTTTGAATTTCTTTTAAAGAACTGAGGTTTCAATACATACCATGGAATA 3240
QY 3241 ATCTTACTTTTCTTGTACTACAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAG 3300
Db 3241 ATCTTACTTTTCTTGTACTACAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAG 3300
QY 3301 GCGAGGTTGTACTATATGACATATCAAT 3330
Db 3301 GCGAGGTTGTACTATATGACATATCAAT 3330
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## RESULT 3

AAA46205  
ID AAA46205 standard; cDNA; 3263 BP.

XX AAA46205;

DT 04-SEP-2000 (first entry)

XX cDNA encoding an interphotoreceptor matrix proteoglycan (IPMI50).

XX Interphotoreceptor matrix; IPM; proteoglycan; IPMI50; IPMC; IPM200;  
XX chromosome 6q13-q15; ocular disease; retinal detachment;  
XX choriorretinal degeneration; retinal degeneration; cone degeneration;  
XX age related macular degeneration; photoreceptor degeneration;  
XX retinal pigment epithelium degeneration; mucopolysaccharidosis;  
XX rod- cone dystrophy; cone-rod dystrophy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 128..244

XX /tag= a

XX /transl\_except= (pos: 2411..2414, aa: Lys)

XX /product= "interphotoreceptor matrix proteoglycan IPMI50"

XX WO200026367-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025440.

XX 29-OCT-1998; 98US-00193972.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2000-365616/31.

XX P-PSDB; AAY93336.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for

PT preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and chorioretinal degeneration.

XX Claim 2; Fig 3; 183pp; English.

XX  
 CC The present sequence encodes an interphotoreceptor matrix (IPM)  
 CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).  
 CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
 CC is located on chromosome 6q13-q15, between markers CHLC.GAT11F10 and  
 CC D6S284. The IPM proteins may be used to supplement a patient's own  
 CC production of the protein or to rectify alterations in their nucleic  
 CC acids that result in expression of an inactive protein. The IPM nucleic  
 CC acids may be used in this way to treat ocular diseases such as retinal  
 CC detachment, chorioretinal degeneration, retinal degeneration, age related  
 CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
 CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
 CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
 CC also be used to assay for other modulators of IPM proteoglycan expression  
 CC and activity that may be used to treat ocular diseases. The nucleic acids  
 CC and proteins may also be used as diagnostic reagents to detect the  
 CC presence of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies

XX Sequence 3263 BP; 1040 A; 721 C; 663 G; 938 T; 0 U; 1 Other;

Query Match 93.9%; Score 3125.6; DB 3; Length 3263;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 3257; Conservative 0; Mismatches 5; Indels 69; Gaps 6;

QY	1	TAAACCAAGAGTTATCTCAATCATCTGGTATCAATATATAATATTTTTCACATTTC	60
DB	1	TAAACCAAGAGTTATCTCAATCATCTGGTATCAATATATAATATTTTTCACATTTC	58
QY	61	TGTTACTTTTAAAGAGATTGAGTTGTTCTGTGATTGTTATCAGAATTACCAATGCAC	120
DB	59	TGTTACTTTTAAAGAGATTGAGTTGTTCTGTGATTGTTATCAGAATTACCAATGCAC	117
QY	121	AAAGCCGAGATGTTATTCGAACTAGAGACTATTTTGGTTTTCGATTTCCTCA	180
DB	118	AAAGCCGAGATGTTATTCGAACTAGAGACTATTTTGGTTTTCGATTTCCTCA	177
QY	181	AGTTCAAGGAACCAAGATATCTTCAATTAACATATACCAATCTGAACTAAAGACATAGA	240
DB	178	AGTTCAAGGAACCAAGATATCTTCAATTAACATATACCAATCTGAACTAAAGACATAGA	237
QY	241	CAATCCCCAAGAAATGAACAACTGAAAGTACTGAAATAATGTACAAATGTCAACTAT	300
DB	238	CAATCCCCAAGAAATGAACAACTGAAAGTACTGAAATAATGTACAAATGTCAACTAT	297
QY	301	GAGACGAATATTCGATTTCGCAAGCATCGAACAAAGATCCGATTTTCCCAACGGG	360
DB	298	GAGACGAATATTCGATTTCGCAAGCATCGAACAAAGATCCGATTTTCCCAACGGG	357
QY	361	GGTTAAAGTCTGTCACAGAAATCCATGAACACAGATTTTACAGATCTTCAAGCTTATA	420
DB	358	GGTTAAAGTCTGTCACAGAAATCCATGAACACAGATTTTACAGATCTTCAAGCTTATA	417
QY	421	TAGATTGAGAGTGTGTCAGAGACATATGGGAAGCATATCGATCTTCTGGATCGCAT	480
DB	418	TAGATTGAGAGTGTGTCAGAGACATATGGGAAGCATATCGATCTTCTGGATCGCAT	477
QY	481	CCCTGACACAGGGGAATATCAGAGCTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGGCT	540
DB	478	CCCTGACACAGGGGAATATCAGAGCTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGGCT	537
QY	541	CTTTGACATGTGAAATACTTCAGAAATTCACAGAGCACTTGGATCTTCTCCACAGAG	600
DB	538	CTTTGACATGTGAAATACTTCAGAAATTCACAGAGCACTTGGATCTTCTCCACAGAG	597
QY	601	AATAAACACAGAGAGTTTCCCTGCACAGAAAGATGAATATCTGCAGAGAGACATTTGGG	660
DB	598	AATAAACACAGAGAGTTTCCCTGCACAGAAAGATGAATATCTGCAGAGAGACATTTGGG	657

QY	661	AGACCTGGTGAACACATTGTCATTTTCAACAGCAATCTACATTTCAAGAGACTTTGGGCAGT	720
DB	658	AGACCTGGTGAACACATTGTCATTTTCAAC	687
QY	721	ATTCTAAGAAACCCCTCAGAGAGCAAAATTCAGAGATTTGCCAACGCTTCACTTGGGCCT	780
DB	688	-----AGATGTTGCCAACGCTTCACTTGGGCCT	715
QY	781	TTCCCTCTCACTCTGATGACACCCCTCAATGAATTTCTCGATATATACACTCAACGAC	840
DB	716	TTCCCTCTCACTCTGATGACACCCCTCAATGAATTTCTCGATATATACACTCAACGAC	775
QY	841	ACCAAGATGCTCAACACAGAAAGAGAAACAGAAATTCGCTGTGTTGGAGGACGAGGGTG	900
DB	776	ACCAAGATGCTCAACACAGAAAGAGAAACAGAAATTCGCTGTGTTGGAGGACGAGGGTG	835
QY	901	GAGCTCAGCTCTCTCTGTTAAACAGAGTTTCAAGCAGAGCTCGTGAATCCAGTCC	960
DB	836	GAGCTCAGCTCTCTCTGTTAAACAGAGTTTCAAGCAGAGCTCGTGAATCCAGTCC	895
QY	961	CCATATTACCAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAAA	1020
DB	896	CCATATTACCAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAAA	955
QY	1021	CTTCCAGGATTCAAAATAATTCATGTTAGGATTTAGACCAAGAAAGAAAGATGGC	1080
DB	956	CTTCCAGGATTCAAAATAATTCATGTTAGGATTTAGACCAAGAAAGAAAGATGGC	1015
QY	1081	TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAAGCAAAA	1140
DB	1016	TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAAGCAAAA	1075
QY	1141	AGCCTCAAGTCACTCTCTGTTTGAATTCACAAAATTTGAAAGTGAAGGAGTCTAT	1200
DB	1076	AGCCTCAAGTCACTCTCTGTTTGAATTCACAAAATTTGAAAGTGAAGGAGTCTAT	1135
QY	1201	CATGGACCATGTGAGGAGGACACAGCAATCTATCTCACACTACAGACCTCAAA	1260
DB	1136	CATGGACCATGTGAGGAGGACACAGCAATCTATCTCACACTACAGACCTCAAA	1195
QY	1261	AGGCTGATCAGCAAGACCTAGAGGAGAACCAATCTTTGGATGTGGGCAATTCAGTTC	1320
DB	1196	AGGCTGATCAGCAAGACCTAGAGGAGAACCAATCTTTGGATGTGGGCAATTCAGTTC	1255
QY	1321	ACTGATGAATTTCTGATCAGTCCAGCCTTTGGTCTTGACACCCCAATCAGAGCTGCC	1380
DB	1256	ACTGATGAATTTCTGATCAGTCCAGCCTTTGGTCTTGACACCCCAATCAGAGCTGCC	1315
QY	1381	ACATCTTTTCTGTTATACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAA	1440
DB	1316	ACATCTTTTCTGTTATACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAA	1375
QY	1441	CCCCAGCTTGAGACAGTGGACGAGCAGAGCATGGTCTTACCTGACACTTCTTGGTCTCCA	1500
DB	1376	CCCCAGCTTGAGACAGTGGACGAGCAGAGCATGGTCTTACCTGACACTTCTTGGTCTCCA	1435
QY	1501	CCTGCTATGCTCTACCTCCCTGTGAGAGGCTCCACCTTTCTTTATGGCATCAAGCATC	1560
DB	1436	CCTGCTATGCTCTACCTCCCTGTGAGAGGCTCCACCTTTCTTTATGGCATCAAGCATC	1495
QY	1561	TTCTCTGTGATCAAGGACCAACAGATACAAATGCCACTGACCAACAATGCTAGTA	1620
DB	1496	TTCTCTGTGATCAAGGACCAACAGATACAAATGCCACTGACCAACAATGCTAGTA	1555
QY	1621	CCAGGCTCAGCATCCCAACAGTATTTCTGCAATCAGCAACTGCTCTGGAAAT	1680
DB	1556	CCAGGCTCAGCATCCCAACAGTATTTCTGCAATCAGCAACTGCTCTGGAAAT	1615
QY	1681	TCACATCCACCTGATCTTTCAGATGACGCGCATCAAGTGCAGGTGGGAAAGATATGGTC	1740
DB	1616	TCACATCCACCTGATCTTTCAGATGACGCGCATCAAGTGCAGGTGGGAAAGATATGGTC	1675
QY	1741	AGACACCTAGATGAATGGATCTGCTCTGACACTCTGCTGCCCATCTCAGGATACCAGAGCTC	1800

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Db 1676 AGACACCTAGATGAATGGATCTGTCTGACACTCTGCCCATCTGAGGTACAGAGCTC 1735
QY 1801 AGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGGATACCACTCTCTGTCTCAGCTTTA 1860
Db 1736 AGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGGATACCACTCTCTGTCTCAGCTTTA 1795
QY 1861 CAGTATATACCACTAGTCTTATGACCATTTGCCCAAGGGCCGAGAGCTGGTAGTGTC 1920
Db 1796 CAGTATATACCACTAGTCTTATGACCATTTGCCCAAGGGCCGAGAGCTGGTAGTGTC 1855
QY 1921 TTCACTCTGGTGTGCTTAACATGGGCTTCTCCACGAGCTCTGTTCAACAGAGCTCTCTG 1980
Db 1856 TTCACTCTGGTGTGCTTAACATGGGCTTCTCCACGAGCTCTGTTCAACAGAGCTCTCTG 1915
QY 1981 GAGTACCGAGCTCTGGAGCAACAATTCACAGCTCTCTGGTCTCCATATCTAGATCCCAAT 2040
Db 1916 GAGTACCGAGCTCTGGAGCAACAATTCACAGCTCTCTGGTCTCCATATCTAGATCCCAAT 1975
QY 2041 CTTACAGGATTTAAGCAACTTGAATACCTTAACCTTCAGAAACGGGAGTGTGATGTAAT 2100
Db 1976 CTTACAGGATTTAAGCAACTTGAATACCTTAACCTTCAGAAACGGGAGTGTGATGTAAT 2035
QY 2101 AGCAAAATGAAGTTTCTGAAGTCTGTGCGGTATTAACCTCACCAGGCTGTGACGGGTC 2160
Db 2036 AGCAAAATGAAGTTTCTGAAGTCTGTGCGGTATTAACCTCACCAGGCTGTGACGGGTC 2095
QY 2161 TTGAGGATTTTCTGCTCTGAGCCCAACAACTCCATCTCGAAATAGACAGCTACTCT 2220
Db 2096 TTGAGGATTTTCTGCTCTGAGCCCAACAACTCCATCTCGAAATAGACAGCTACTCT 2155
QY 2221 CTCACATTTGAACCGCTGATCAAGCAGATCCGTGCAAGTTCCTGGCTGGCGCAATTT 2280
Db 2156 CTCACATTTGAACCGCTGATCAAGCAGATCCGTGCAAGTTCCTGGCTGGCGCAATTT 2215
QY 2281 GCCCAATGTGTAAGAAACCAACGGACTGAGGAAGCGGAGTGTGCTGCAAAACCCAGGATAT 2340
Db 2216 GCCCAATGTGTAAGAAACCAACGGACTGAGGAAGCGGAGTGTGCTGCAAAACCCAGGATAT 2275
QY 2341 GACAGCAGGGAGCTGGAACGGTCTGGAACCAAGCCCTCTGTGGCCCTGGCACAAGGAA 2400
Db 2276 GACAGCAGGGAGCTGGAACGGTCTGGAACCAAGCCCTCTGTGG--CTTGGCACAAGGAA 2334
QY 2401 TCCGAGGTCTCTCAGGGAAGGGGCTCCATGCGAGTTGCCAGATCATCTCTGAAATCAA 2460
Db 2335 TCCGAGGTCTCTCAGGGAAGGGGCTCCATGCG--GGTTCAGATCATCTCTGAAATCAA 2392
QY 2461 GCATACAAAACCTAGTGTGTTAAAAAGTTCCAAAATCAACAAAATAACAAGGTAAATCAGTAAA 2520
Db 2393 GCATACAAAACCTAGTGTGTTAAAAAGTTCCAAAATCAACAAAATAACAAGGTAAATCAGTAAA 2452
QY 2521 AGAAATTTCTGAATTA-CTGACCGTAGAATATGAGAAATTTAACCATCAAGATTGGGAAGG 2579
Db 2453 AGAAATTTCTGAATTA-CTGACCGTAGAATATGAGAAATTTAACCATCAAGATTGGGAAGG 2512
QY 2580 AAATTAATAAATCTGAAAATGTACAAATATATCACTTAGGCTATCTCAAGAGAGATGATTGGC 2639
Db 2513 AAATTAATAAATCTGAAAATGTACAAATATATCACTTAGGCTATCTCAAGAGAGATGATTGGC 2572
QY 2640 TTCTCAAGGAAAATGGAGACAGGCAATATTCATGGGTATCAAAAATCCAGACATACAGTCA 2699
Db 2573 TTCTCAAGGAAAATGGAGACAGGCAATATTCATGGGTATCAAAAATCCAGACATACAGTCA 2632
QY 2700 ACACGTGAGAATCAGCACACACATATTTCAATATAGAGAGTCAATGTTGGCAACCA 2759
Db 2633 ACACGTGAGAATCAGCACACACATATTTCAATATAGAGAGTCAATGTTGGCAACCA 2692
QY 2760 GTAAATTTGAAAAAAGACACCTTACTTATTAATAAACCACCAATCAATCAGCGAAA 2819
Db 2693 GTAAATTTGAAAAAAGACACCTTACTTATTAATAAACCACCAATCAATCAGCGAAA 2752
QY 2820 CATATTTTATCTATCTTGGATGATAGTCAAAATGATCAAGCCAGGTTTGTCTCCACC 2879
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Db 2753 CATATTTTATCTATCTTGGATGATGATCAAAATGATCATAAGCCAGGTTTGTCTCCACC 2812
QY 2880 TTCCCTGAAAAATTTTACTCACAGATCATTTTGCACCAAGCATAGCTTACTTATTGTTAGG 2939
Db 2813 TTCCCTGAAAAATTTTACTCACAGATCATTTTGCACCAAGCATAGCTTACTTATTGTTAGG 2872
QY 2940 GACTGAAACAATTTATTTGGGAGCAAACTCTTTATATGCTAGAAAAGTACATTTAAAAGATG 2999
Db 2873 GACTGAAACAATTTATTTGGGAGCAAACTCTTTATATGCTAGAAAAGTACATTTAAAAGATG 2932
QY 3000 ACTACTTACGAGGAGATGAGGCTCTCTCTAAACCGCATGAATGATGTTAGTGTGTTAGGC 3059
Db 2933 ACTACTTACGAGGAGATGAGGCTCTCTCTAAACCGCATGAATGATGTTAGTGTGTTAGGC 2992
QY 3060 ACTGAGTGTGATATATATGCTCCACACTAGTCTCTGATAAACACAAACCTCAGTATTCA 3119
Db 2993 ACTGAGTGTGATATATATGCTCCACACTAGTCTCTGATAAACACAAACCTCAGTATTCA 3052
QY 3120 GTTATTAGGCACACTAGTCTTTTATACGCAACTACTGCTTACATAGTACAGTGTGTTGTC 3179
Db 3053 GTTATTAGGCACACTAGTCTTTTATACGCAACTACTGCTTACATAGTACAGTGTGTTGTC 3112
QY 3180 CAATPAATCTTTGAAATGTTCTTTTAAAGAAACTGAGTTCAGATACACATACCATGGA 3239
Db 3113 CAATPAATCTTTGAAATGTTCTTTTAAAGAAACTGAGTTCAGATACACATACCATGGA 3172
QY 3240 AATCTTACTTTTCTGTTTACTACACAAAGCTATTTTAAAGAAAGTCTATGTTGGGAGAA 3299
Db 3173 AATCTTACTTTTCTGTTTACTACACAAAGCTATTTTAAAGAAAGTCTATGTTGGGAGAA 3232
QY 3300 GGGCGAAGTTGTACTATATGACATAATCAAT 3330
Db 3233 GGGCGAAGTTGTACTATATGACATAATCAAT 3263

RESULT 4
ID ADA14866 standard; cdna; 3261 BP.
XX AC ADA14866;
XX AC AC
XX DT 06-NOV-2003 (first entry)
XX XX
DE Human cDNA encoding variant IPMC 150 isoform A.
XX XX
KW ss; gene; human; IPMC 150 isoform A; gene therapy;
KW interphotoreceptor matrix component; IPMC; ocular disorder;
KW macular degeneration; photoreceptor death; retinal detachment.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 128..2443
FT FT /*tag= a
FT FT /product= "Variant IPMC 150 isoform A"
XX XX
PN US2002160954-A1.
XX XX
PD 31-OCT-2002.
XX XX
PF 08-NOV-2001; 2001US-00007270.
XX XX
PR 29-OCT-1998; 98US-00183972.
PR 29-OCT-1999; 99US-00430195.
XX XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX XX
PI Hageman GS, Kuehn MH;
XX XX
DR WPI; 2003-238235/23.
DR P-FSDB; ADA14867.
XX XX
PT New isolated or recombinant interphotoreceptor matrix component
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QY 1861 CAGTATATCACCACTAGTTCTATGACCAATGCCCCAAGCGCGAGAGCTGGTAGTGTTC 1920  
Db 1796 CAGTATATCACCACTAGTTCTATGACCAATGCCCCAAGCGCGAGAGCTGGTAGTGTTC 1855  
QY 1921 TTGAGTCTGGGTGTGTAAATGCGCTTCTCAACGACCTGTTCACCAAGAGAGCTCTCTG 1980  
Db 1856 TTGAGTCTGGGTGTGTAAATGCGCTTCTCAACGACCTGTTCACCAAGAGAGCTCTCTG 1915  
QY 1981 GAGTACCGAGCTCTGGAGCAACAAATTCACACAGCTGTGTTCCATATCTACGATCCAAT 2040  
Db 1916 GAGTACCGAGCTCTGGAGCAACAAATTCACACAGCTGTGTTCCATATCTACGATCCAAT 1975  
QY 2041 CTTACAGGATTTAAGCAACTTGAATTAATCTTAACTTCAGAAACGGGAGTGTGATTTGTAAT 2100  
Db 1976 CTTACAGGATTTAAGCAACTTGAATTAATCTTAACTTCAGAAACGGGAGTGTGATTTGTAAT 2035  
QY 2101 AGCAAAATGAAGTTGCTAGTCTGTGCGGTATTAACCTTCAACAGGCTGTGACGGGGTC 2160  
Db 2036 AGCAAAATGAAGTTGCTAGTCTGTGCGGTATTAACCTTCAACAGGCTGTGACGGGGTC 2095  
QY 2161 TTGGAGGATTTTGGTCTGTGTCAGGCCCAACCACTCCATCTGGAATAGACAGCTACTCT 2220  
Db 2096 TTGGAGGATTTTGGTCTGTGTCAGGCCCAACCACTCCATCTGGAATAGACAGCTACTCT 2155  
QY 2221 CTCACGATTTGAACCACTGATCAAGCAGATCCCTGCAAGTTCCTGGCCTGCGGCGAATTT 2280  
Db 2156 CTCACGATTTGAACCACTGATCAAGCAGATCCCTGCAAGTTCCTGGCCTGCGGCGAATTT 2215  
QY 2281 GCCCAATGTGTAAGAACGAGCGAGCTGAGGAAGCGGAGTGTGCTGCAACCAAGATAT 2340  
Db 2216 GCCCAATGTGTAAGAACGAGCGAGCTGAGGAAGCGGAGTGTGCTGCAACCAAGATAT 2275  
QY 2341 GACAGCGAGGGAGCTGGAACCGTCTGGAACCAAGGCTCTGTGGCCTGGCAACAAAGGAA 2400  
Db 2276 GACAGCGAGGGAGCTGGAACCGTCTGGAACCAAGGCTCTGTGGCCTGGCAACAAAGGAA 2334  
QY 2401 TGGAGGCTCTCCAGGGAAGGAGCTCCATGAGGTTGCCAGATCACTGTGAAATCAA 2460  
Db 2335 TGGAGGCTCTCCAGGGAAGGAGCTCCATGAGGTTGCCAGATCACTGTGAAATCAA 2392  
QY 2461 GCATACAAACTAGTGTAAAAAGTTTCCAAATCAACAAATTAACAAGGTATCAAGTAAA 2520  
Db 2393 GCATACAAACTAGTGT - ABAAGTTCCAAATCAACAAATTAACAAGGTATCAAGTAAA 2451  
QY 2521 AGAAATTCGAATTACTGACCGTAGAATATGAAGAAATTTAACATCAAGATTTGGGAAGGA 2580  
Db 2452 AGAAATTCGAATTACTGACCGTAGAATATGAAGAAATTTAACATCAAGATTTGGGAAGGA 2511  
QY 2581 AATTAAAACTGAAATGTACAAATATCACTTAGGCTATCTCAAGAGAGATGATTTGGCT 2640  
Db 2512 AATTAAAACTGAAATGTACAAATATCACTTAGGCTATCTCAAGAGAGATGATTTGGCT 2571  
QY 2641 TCTCAAGGAAATGGAGACAGGCATATTCATGGGTTCATCAAAATCCAGACATACAGTCAA 2700  
Db 2572 TCTCAAGGAAATGGAGACAGGCATATTCATGGGTTCATCAAAATCCAGACATACAGTCAA 2631  
QY 2701 CACTGAGATCAGCACACACCATATTTCAAATATAGAGAGTCATGTACTTGGCAACAG 2760  
Db 2632 CACTGAGATCAGCACACACCATATTTCAAATATAGAGAGTCATGTACTTGGCAACAG 2691  
QY 2761 TAAATTTGAAAAAAGACACTTACTTATTTATTTAAAAACCCCAATGCAATCAGCGAAAC 2820  
Db 2692 TAAATTTGAAAAAAGACACTTACTTATTTATTTAAAAACCCCAATGCAATCAGCGAAAC 2751  
QY 2821 ATATTTTACTATTTCTGATGATAGTCAAATGATATCAAGCGAGTTGCTTCCACCT 2880  
Db 2752 ATATTTTACTATTTCTGATGATAGTCAAATGATATCAAGCGAGTTGCTTCCACCT 2811  
QY 2881 TCCCTGAAATTTTACTCAGATCATTTTGAACCAAGCATAGCTTACTTATTTGTTAGG 2940  
Db 2812 TCCCTGAAATTTTACTCAGATCATTTGCAACCAAGCATAGCTTACTTATTTGTTAGG 2871

QY 2941 ACTGAACAATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000  
Db 2872 ACTGAACAATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 2931  
QY 3001 CTACTTACGAGGAGATGACAGTCTCTCTAAACGCAATGAATGATGTAGTGTGAGGCA 3060  
Db 2932 CTACTTACGAGGAGATGACAGTCTCTCTAAACGCAATGAATGATGTAGTGTGAGGCA 2991  
QY 3061 CTGTAGTGAAGTGTATATATGCTCCACACTACTGCTGATATAACACAAAACCTCAGTATTCA 3120  
Db 2992 CTGTAGTGAAGTGTATATATGCTCCACACTACTGCTGATATAACACAAAACCTCAGTATTCA 3051  
QY 3121 TTATTAGGCACACTAGTTTATATAGCAACTACTGCTTACATAGTAGACTGTTTGTGGCC 3180  
Db 3052 TTATTAGGCACACTAGTTTATATAGCAACTACTGCTTACATAGTAGACTGTTTGTGGCC 3111  
QY 3181 AATAATCTTTGAAATGTTCTTTTAAAGAACTGAGGTTTCAGATACACATACCATGGAAAA 3240  
Db 3112 AATAATCTTTGAAATGTTCTTTTAAAGAACTGAGGTTTCAGATACACATACCATGGAAAA 3171  
QY 3241 ATCTTACTTTTCTGTTTACTACACAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAAG 3300  
Db 3172 ATCTTACTTTTCTGTTTACTACACAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAAG 3231  
QY 3301 GCGAAGTTGTACTATATGACATAATCAAT 3330  
Db 3232 GCGAAGTTGTACTATATGACATAATCAAT 3261

RESULT 5  
ACCS7960  
ID ACCS7960 standard; cDNA; 3261 BP.  
XX AC ACCS7960;  
XX AC  
XX DT 11-AUG-2003 (first entry)  
XX DE Human interphotoreceptor matrix IPM 150, isoform A variant, cDNA.  
XX HU Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
XX KW receptor; ophthalmological; gene therapy; gene; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 128..2443  
XX FT /\*tag= a  
XX FT /product= "IPM 150"  
XX  
XX DN WO2003039346-A2.  
XX  
XX PD 15-MAY-2003.  
XX  
XX PF 08-NOV-2002; 2002WO-US036090.  
XX PR 08-NOV-2001; 2001US-00077270.  
XX  
XX PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX PI Hageman GS, Kuehn MH;  
XX  
XX DR WPI; 2003-441440/41.  
XX DR P-PSDB; ABR42354.  
XX  
XX PT New interphotoreceptor matrix proteins and polynucleotides, useful for  
XX PT treating or preventing photoreceptor death or retinal detachment, or for  
XX PT treating ocular disorders.  
XX  
XX PS Claim 1; Page 91-94; 105pp; English.  
XX  
XX CC The present sequence is that of cDNA encoding a variant of isoform A of  
XX CC novel human interphotoreceptor matrix 150 (IPM 150), a member of the  
XX CC newly identified interphotoreceptor matrix component (IPMC) gene family.



Db 1796 CAGTATATCACCACTAGTCTTATGACCATTTGCCCCCAAGGCCGAGAGCTGTAGTGTTC 1955  
Qy 1921 TTCAAGTCTGGGTGTCTAATAGTCCCTTCTCCAAAGACCTGTTCACAAAGAGCTCTCTG 1980  
Db 1956 TTCAAGTCTGGGTGTCTAATAGTCCCTTCTCCAAAGACCTGTTCACAAAGAGCTCTCTG 1915  
Qy 1981 GAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGTCTGTTCCATATCTACCATCAAT 2040  
Db 1916 GAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGTCTGTTCCATATCTACCATCAAT 1975  
Qy 2041 CTTACAGGATTTAAGCACTTGAATCTTAACTTCAAGAAACGGGAGTGATTTGGAAT 2100  
Db 1976 CTTACAGGATTTAAGCACTTGAATCTTAACTTCAAGAAACGGGAGTGATTTGGAAT 2035  
Qy 2101 AGCAAAATGAAGTTTGTCTAGTCTGTCCGTATAAACCCTCACCAGGCTGTGACGGGTC 2160  
Db 2036 AGCAAAATGAAGTTTGTCTAGTCTGTCCGTATAAACCCTCACCAGGCTGTGACGGGTC 2095  
Qy 2161 TTGAGGATTTTGTCTGTCTGAGCCCAACAACCTCCATCTGGAATAGACAGCTACTCT 2220  
Db 2096 TTGAGGATTTTGTCTGTCTGAGCCCAACAACCTCCATCTGGAATAGACAGCTACTCT 2155  
Qy 2221 CTCAACATTCGACAGCTGATCAAGCAGATCCCTGCMAGTTCTGGCCTGGCGGCAATTT 2280  
Db 2156 CTCAACATTCGACAGCTGATCAAGCAGATCCCTGCMAGTTCTGGCCTGGCGGCAATTT 2215  
Qy 2281 GCCCAATGTGTAAGAACGAGCTGAGCAAGCGAGTGTCTGCTGCAAAACAGGATAT 2340  
Db 2216 GCCCAATGTGTAAGAACGAGCTGAGCAAGCGAGTGTCTGCTGCAAAACAGGATAT 2275  
Qy 2341 GACAGCCAGGGAGCTGGACGCTGTGGAAACAGGCTCTGTGGCCCTGGCAAAAGGAA 2400  
Db 2276 GACAGCCAGGGAGCTGGACGCTGTGGAAACAGGCTCTGTGG--CCTGGCAAAAGGAA 2334  
Qy 2401 TGGGAGTCTCTCAGGAAAGGAGCTCCATGTCAGAGTTCAGATCAGCTCAAAATCAA 2460  
Db 2335 TGGGAGTCTCTCAGGAAAGGAGCTCCATG--GGTTCAGATCAGCTCAAAATCAA 2392  
Qy 2461 GCATACAAAATAGTGTAAAAAGTTTCCAAAATCAACAAAATAACAAAGTAAATCAAGTAAA 2520  
Db 2393 GCATACAAAATAGTGT--AAAAGTTTCCAAAATCAACAAAATAACAAAGTAAATCAAGTAAA 2451  
Qy 2521 AGAAATCTGAATCTGACCGTAGAATATGAAGATTTAAACATCAAGATTTGGGAAGA 2580  
Db 2452 AGAAATCTGAATCTGACCGTAGAATATGAAGATTTAAACATCAAGATTTGGGAAGA 2511  
Qy 2581 AATTAAAACTGAAAATGTACAAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCT 2640  
Db 2512 AATTAAAACTGAAAATGTACAAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCT 2571  
Qy 2641 TCTCAAGGAAATGGAGACAGGATATTCATGGGTATCAAAATCCAGCATACAGTCAA 2700  
Db 2572 TCTCAAGGAAATGGAGACAGGATATTCATGGGTATCAAAATCCAGCATACAGTCAA 2631  
Qy 2701 CACTGAGATCAGCACACACCATATTTCAAAATATAGAGATCATGTACTTGGCAACAG 2760  
Db 2632 CACTGAGATCAGCACACACCATATTTCAAAATATAGAGATCATGTACTTGGCAACAG 2691  
Qy 2761 TAAATCTGAAAAAAGACACTTACTTATTATTAACCCCAATGCAATCAGCGAAAC 2820  
Db 2692 TAAATCTGAAAAAAGACACTTACTTATTATTAACCCCAATGCAATCAGCGAAAC 2751  
Qy 2821 ATATTTTACTATTTCTGATATAGTCAAAATGATCATAGCCAGGTTTGTCCACCT 2880  
Db 2752 ATATTTTACTATTTCTGATATAGTCAAAATGATCATAGCCAGGTTTGTCCACCT 2811  
Qy 2881 TCCTGAAATTTTACTCACAGATCATTTGCAACAGATAGCTTACTTATTATTGTTAGG 2940  
Db 2812 TCCTGAAATTTTACTCACAGATCATTTGCAACAGATAGCTTACTTATTATTGTTAGG 2871  
Qy 2941 ACTGAAATTTTATTGGGAAGCAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000

Db 2872 ACTGAACAAATTTNTTGGAGCAAACTCTTATATGCTAGAAAGTACATTTAAAGATGA 2931  
Qy 3001 CTACTTACGCGAGGAGATGCGAGTCTCTCTAAACGCAATGAATGTATGTGTAGGCA 3060  
Db 2932 CTACTTACGCGAGGAGATGCGAGTCTCTCTAAACGCAATGAATGTATGTGTAGGCA 2991  
Qy 3061 CTGTAGTCAAGTGTATATATGCTCCACACTAGCTCTGATTAACACAAACCTCAGTATTCAG 3120  
Db 2992 CTGTAGTCAAGTGTATATATGCTCCACACTAGCTCTGATTAACACAAACCTCAGTATTCAG 3051  
Qy 3121 TTATTAGGCACACTAGTATTTTATAGCAACTACTCTTACATAGTAGAGCTGTTTGTGGCC 3180  
Db 3052 TTATTAGGCACACTAGTATTTTATAGCAACTACTCTTACATAGTAGAGCTGTTTGTGGCC 3111  
Qy 3181 AATAATCTTGAATTTGTTTAAAGAACTGAGGTTTCAGATACATACCATGGGAAA 3240  
Db 3112 AATAATCTTGAATTTGTTTAAAGAACTGAGGTTTCAGATACATACCATGGGAAA 3171  
Qy 3241 ATCTTACTTTTCTTGTACTACACAAAGCTATTTTAAAGAAAGATGCTATGTTGGAGAG 3300  
Db 3172 ATCTTACTTTTCTTGTACTACACAAAGCTATTTTAAAGAAAGATGCTATGTTGGAGAG 3231  
Qy 3301 GCGGAGTTGTACTATATGACATAATCAAT 3330  
Db 3232 GCGGAGTTGTACTATATGACATAATCAAT 3261

RESULT 6  
ADA14842  
ID ADA14842 standard; cDNA; 2887 BP.  
XX  
AC ADA14842;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.  
XX  
KW ss; gene; human; IPMC 150 isoform B; gene therapy;  
interphotoreceptor matrix component; IPMC; ocular disorder;  
macular degeneration; photoreceptor death; retinal detachment.  
XX  
OS Homo sapiens.  
XX  
FH Key  
CDS Location/Qualifiers  
FT 5..2143  
FT /\*tag= a  
FT /partial  
FT /product= "IPMC 150 isoform B"  
FT /notes= "No start codon given. Encodes residues 8-719 of  
(seqid:4)"  
XX  
FN US2002160954-A1.  
XX  
PD 31-OCT-2002.  
XX  
PF 08-NOV-2001; 2001US-00007270.  
XX  
PR 29-OCT-1998; 98US-00183972.  
PR 29-OCT-1999; 99US-00430195.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Hageman GS, Kuehn MH;  
XX  
DR WPI; 2003-238235/23.  
DR P-PSDB; ADA14843.  
XX  
PT New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
or retinal detachment.  
XX  
PS Claim 3; Page 33-34; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding human  
CC interphotoreceptor matrix component, IPMC, 150 isoform B.

XX SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

Query Match 83.1%; Score 2765.8; DB 7; Length 2887;

Best Local Similarity 97.1%; Pred. No. 0;

Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;

QY	396	TTTTAGACAGCTTTCAAGCTTATTATAGATTGAGAGTGTCTCAGGAGCAGTATGGGAAG	455
DB	15	TTTTTTGGATTTTCTCCAGTTCAAGGAACCAAGTGTCTCAGGAAGCAGTATGGGAAG	74
QY	456	CATATCGGATTTTCTGGATCGCATCCCTGCACACAGGGGAATATCAGGACTGGGTGAGCA	515
DB	75	CATATCGGATTTTCTGGATCGCATCCCTGCACACAGGGGAATATCAGGACTGGGTGAGCA	134
QY	516	TCTGCCACGAGGAGACCTTCTGCTCTTTTGACATTTGGAAAAAATTTTCTCAGCAATTTCCGAGG	575
DB	135	TCTGCCACGAGGAGACCTTCTGCTCTTTTGACATTTGGAAAAAATTTTCTCAGCAATTTCCGAGG	194
QY	576	AGCATTGGATTTTCTCCAGCAGAGATATAACAGAGAGTTTCCCTGCACAGAAAAGATG	635
DB	195	AGCATTGGATTTTCTCCAGCAGAGATATAACAGAGAGTTTCCCTGCACAGAAAAGATG	254
QY	636	AAATATCTGCAGAGAGACATTTGGGAGAGCTGTGTGAACCATTTGTCATTTCAACAGCAA	695
DB	255	AAATATCTGCAGAGAGACATTTGGGAGAGCTGTGTGAACCATTTGTCATTTCAAC	309
QY	696	TCTACATTTCAAGACTTTGGGAGTATTTCTAAGAAACCCCTCAGAGAGCAAAATTCAGA	755
DB	310	-----AGG	312
QY	756	TGTTGCCAAGCTTCTACCTTGGGCTTTCCCTCTCACTCTCCTGATGACACCTCTCTCAATGA	815
DB	313	TGTTGCCAAGCTTCTACCTTGGGCTTTCCCTCTCACTCTCCTGATGACACCTCTCTCAATGA	372
QY	816	AATTTCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAAAGAGAAACAGAAAT	875
DB	373	AATTTCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAAAGAGAAACAGAAAT	432
QY	876	CGCTGTGTTGGAGAGCAGAGGTTGGAGCTCAGCGTCTCTCTGGTAAACCGAGAGTTCAA	935
DB	433	CGCTGTGTTGGAGAGCAGAGGTTGGAGCTCAGCGTCTCTCTGGTAAACCGAGAGTTCAA	492
QY	936	GGCAGAGCTCGCTGACTCCAGTCCCCCATATTACAGGAGCTAGCAGGAAAGTCCCAACT	995
DB	493	GGCAGAGCTCGCTGACTCCAGTCCCCCATATTACAGGAGCTAGCAGGAAAGTCCCAACT	552
QY	996	TCAGATCCAAAAGATATTAAAGAACTTCCAGGATTCAAAATAATCCATGTGTAGGATT	1055
DB	553	TCAGATCCAAAAGATATTAAAGAACTTCCAGGATTCAAAATAATCCATGTGTAGGATT	612
QY	1056	TAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATCAACTTACGGCCATCTT	1115
DB	613	TAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATCAACTTACGGCCATCTT	672
QY	1116	TAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTGACCTCTCTCTTTTGTATCCAA	1175
DB	673	TAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTGACCTCTCTCTTTTGTATCCAA	732
QY	1176	CAAAATTTGAAGTGAAGAGCTTATCATGGAACCATGGAGGAGCAAGCAACCCAGAAAT	1235
DB	733	CAAAATTTGAAGTGAAGAGCTTATCATGGAACCATGGAGGAGCAAGCAACCCAGAAAT	792

QY	1236	CTATCTCAGCTACAGACCTCAAAAGCTGATCAGCAAGACCTAGAGGAGAACAAATC	1295
DB	793	CTATCTCAGCTACAGACCTCAAAAGCTGATCAGCAAGACCTAGAGGAGAACAAATC	852
QY	1296	TTTGATGTGGGACAATTCAGTTCACTGATGAATTCCTGGATCACTGCCAGCTTTGG	1355
DB	853	TTTGATGTGGGACAATTCAGTTCACTGATGAATTCCTGGATCACTGCCAGCTTTGG	912
QY	1356	TCTTCACACCCCAATCAGAGCTGCCACATCTTTTGGCTGTATTAACAGAGGATGCTACTTT	1415
DB	913	TCTTCACACCCCAATCAGAGCTGCCACATCTTTTGGCTGTATTAACAGAGGATGCTACTTT	972
QY	1416	GAGTCCAGAACTTCTCTCTGTGTGAACCCACCTTGAACAGTGAAGAGGAGCAGAGCATG	1475
DB	973	GAGTCCAGAACTTCTCTCTGTGTGAACCCACCTTGAACAGTGAAGAGGAGCAGAGCATG	1032
QY	1476	TCTACTGACACTTCTTGGTCTCCACCTGTCTATGGCTCTTACCTCCCTGTGTCAGAGCTCC	1535
DB	1033	TCTACTGACACTTCTTGGTCTCCACCTGTCTATGGCTCTTACCTCCCTGTGTCAGAGCTCC	1092
QY	1536	ACCTTTCTTTATGGATCAAGCATCTTCTCTGACCTGATCAAGGACCAACAGATACAAAT	1595
DB	1093	ACCTTTCTTTATGGATCAAGCATCTTCTCTGACCTGATCAAGGACCAACAGATACAAAT	1152
QY	1596	GGCCACTGACAGACAATGTGTAGTACAGGGCTCACCATCCCACTCCCACTGATTTCTGC	1655
DB	1153	GGCCACTGACAGACAATGTGTAGTACAGGGCTCACCATCCCACTCCCACTGATTTCTGC	1212
QY	1656	AATCAGCAACTGGCTCTGGGAATTTCACTCCACCTGCTGATCTTCAGATGACAGCCGATC	1715
DB	1213	AATCAGCAACTGGCTCTGGGAATTTCACTCCACCTGCTGATCTTCAGATGACAGCCGATC	1272
QY	1716	AAGTGCAGTGGCGGAAGATATGTCAGACACTAGATGAATGATCTGTCTGACACTCC	1775
DB	1273	AAGTGCAGTGGCGGAAGATATGTCAGACACTAGATGAATGATCTGTCTGACACTCC	1332
QY	1776	TGCCCCATCTCAGGTACAGAGCTCAGCGAATATGTTCTGTCTCCAGATCATTTCTTGA	1835
DB	1333	TGCCCCATCTCAGGTACAGCGGCTCAGCGAATATGTTCTGTCTCCAGATCATTTCTTGA	1392
QY	1836	GGATACACTCTCTCTCAGCTTTTACAGTATATCACCACCTAGTTCTATGACCATGCCCC	1895
DB	1393	GGATACACTCTCTCTCAGCTTTTACAGTATATCACCACCTAGTTCTATGACCATGCCCC	1452
QY	1896	CAAGGGCGAGAGCTGGTAGTGTCTTTCAGTCTCGCTGTTGCTTAACATGGCTTCTCCAA	1955
DB	1453	CAAGGGCGAGAGCTGGTAGTGTCTTTCAGTCTCGCTGTTGCTTAACATGGCTTCTCCAA	1512
QY	1956	CGACTGTTTCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT	2015
DB	1513	CGACTGTTTCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT	1572
QY	2016	GCTGTTCCATATCTACGATCCCAATCTTACAGATTTAAGCACTTCAAACTTAACTT	2075
DB	1573	GCTGTTCCATATCTACGATCCCAATCTTACAGATTTAAGCACTTCAAACTTAACTT	1632
QY	2076	CAGAAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTGCTTAAGTCTGTGCGGTATAA	2135
DB	1633	CAGAAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTGCTTAAGTCTGTGCGGTATAA	1692
QY	2136	CCTCACAAGGCTGTGCACGGGGTCTTGGAGGATTTTCTGCTGTCAGCCCAACAACT	2195
DB	1693	CCTCACAAGGCTGTGCACGGGGTCTTGGAGGATTTTCTGCTGTCAGCCCAACAACT	1752
QY	2196	CCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACACAGCTGATCAAGCAGATCCCTG	2255
DB	1753	CCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACACAGCTGATCAAGCAGATCCCTG	1812
QY	2256	CAAGTCTCGCTCGCGGCAATTTGCCCCAATGTGTAAAGAAAGAGGAGCTGAGGAGC	2315
DB	1813	CAAGTCTCGCTCGCGGCAATTTGCCCCAATGTGTAAAGAAAGAGGAGCTGAGGAGC	1872

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QY 2316 GGAGTGTGCTGCAAAACAGGATATGACAGCCAGGGAGCGTGTGGAACGAG 2375
D 1873 GGAGTGTGCTGCAAAACAGGATATGACAGCCAGGGAGCGTGTGGAACGAG 1932
QY 2376 CCTCTGTGGCCCTGGCAAAAGGAATCGAGTCTCTCAGGAAAGGAGCTCCATGCG 2435
D 1933 CCTCTGTGGCCCTGGCAAAAGGAATCGAGTCTCTCAGGAAAGGAGCTCCATGCG 1992
QY 2436 GTTCCAGATCAGTCTGAAATCAAGATACAAACTAGTGTAAAGATCCAAATCA 2495
D 1993 GTTCCAGATCAGTCTGAAATCAAGATACAAACTAGTGTAAAGATCCAAATCA 2052
QY 2496 ACAAAATACAGTATATGATGAAAGAAATCTGAATTAAGTCTGACCGTAGAATATGAAGA 2555
D 2053 ACAAAATACAGTATATGATGAAAGAAATCTGAATTAAGTCTGACCGTAGAATATGAAGA 2112
QY 2556 ATTTAAACATCAGATGCGGAGGAATTAAGTCTGAAATCAAGTAAATATACATTTACATGAG 2615
D 2113 ATTTAAACATCAGATGCGGAGGAATTAAGTCTGAAATCAAGTAAATATACATTTACATGAG 2172
QY 2616 CTATCTCAAGAGATGATTTGCTCTCAAGGAAATGAGACAGCATATTCATGGGT 2675
D 2173 CTATCTCAAGAGATGATTTGCTCTCAAGGAAATGAGACAGCATATTCATGGGT 2232
QY 2676 CATCAAAATCCAGACATACAGTCAACTGAGATCAGACACACCATATTTCAAAATATA 2735
D 2233 CATCAAAATCCAGACATACAGTCAACTGAGATCAGACACACCATATTTCAAAATATA 2292
QY 2736 GAAGAGTCATGTTACTTGGCAACCAAGTAAATCTGAAAGAAAGACACTTACTTATTA 2795
D 2293 GAAGAGTCATGTTACTTGGCAACCAAGTAAATCTGAAAGAAAGACACTTACTTATTA 2352
QY 2796 AAACCCCAATCAATCAGCAAAACATATTTTACTTATTTTGGATGATGATGATGATGAT 2855
D 2353 AAACCCCAATCAATCAGCAAAACATATTTTACTTATTTTGGATGATGATGATGATGATGAT 2412
QY 2856 TCATAGCAGGCTTCTCCACCTTCCCTGAAATTTTACTTCAAGATCATTTGCAACA 2915
D 2413 TCATAGCAGGCTTCTCCACCTTCCCTGAAATTTTACTTCAAGATCATTTGCAACA 2472
QY 2916 AGCATAGCTTACTTATTTAGGAGTCAACAAATTTATTTGGAGCAAACTCTTTATAT 2975
D 2473 AGCATAGCTTACTTATTTAGGAGTCAACAAATTTATTTGGAGCAAACTCTTTATAT 2532
QY 2976 GCTAGAAAGTACATTTAAAGATGACTTACGACAGGAGATGAGGTCTCTTAAACG 3035
D 2533 GCTAGAAAGTACATTTAAAGATGACTTACGACAGGAGATGAGGTCTCTTAAACG 2592
QY 3036 CATGAATGTATGTAGTGTAGGACCTGTAGTGTATATATGCTCCACACTACGTCT 3095
D 2593 CATGAATGTATGTAGTGTAGGACCTGTAGTGTATATATGCTCCACACTACGTCT 2652
QY 3096 GATAACACAAACCTCAGTATTCAGTATTAAGGACACTAGTATTTATAGCAACTACTGC 3155
D 2653 GATAACACAAACCTCAGTATTCAGTATTAAGGACACTAGTATTTATAGCAACTACTGC 2712
QY 3156 TTACATAGTAGAGTGTGTTGTTGCAATATCTTTGAAATGTTCTTTAAAGAACTAG 3215
D 2713 TTACATAGTAGAGTGTGTTGTTGCAATATCTTTGAAATGTTCTTTAAAGAACTAG 2772
QY 3216 GTTCAGATACATACCATGGAATAATCTTACTTTTCTGTTTACTACAAAGCTATTTT 3275
D 2773 GTTCAGATACATACCATGGAATAATCTTACTTTTCTGTTTACTACAAAGCTATTTT 2832
QY 3276 AAAGAGATGCTATGTTGGAGAGGGGAGTGTGCTATATATGACATATCAAT 3330
D 2833 AAAGAGATGCTATGTTGGAGAGGGGAGTGTGCTATATATGACATATCAAT 2887
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RESULT 7

ACC57947

ID ACC57947 standard; cDNA; 2887 BP.

XX

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AC ACC57947;
XX 11-AUG-2003 (first entry)
XX Human interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX receptor; ophthalmological; gene therapy; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 2..2143
XX FT /*tag= a
XX FT /product= "IPM 150"
XX FT /partial
XX FT /note= "No start codon"
XX PN WO2003039346-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036090.
XX PR 08-NOV-2001; 2001US-00077270.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Hageman GS, Kuehn MH;
XX WP1; 2003-441440/41.
XX PS Claim 1; Page 78-79; 105pp; English.
XX PT New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX Claim 1; Page 78-79; 105pp; English.
XX The present sequence is that of cDNA encoding isoform B of novel human
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 6q13-q15, a region that also contains loci for
XX progressive bifocal choriorretinal atrophy, autosomal dominant Stargardt's
XX -like macular dystrophy, North Carolina macular dystrophy and Salla
XX disease. Members of the IPMC gene family have been identified in humans,
XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or IPM2). The
XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
XX antibodies that specifically bind the polypeptides, and vectors
XX comprising the polynucleotides. A claimed method of treating or
XX preventing photoreceptor death or retinal detachment involves
XX administering an IPMC polynucleotide, polypeptide or antibody. Also
XX claimed is a method for identifying a compound capable of modulating IPMC
XX gene expression
XX Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;
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Query Match 83.1%; Score 2765.8; DB 8; Length 2887;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;
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QY 396 TTTTAGACAGTCTTCAAGCTTATATAGATGAGTGTGTGAGGAGCAGATGGAAG 455
D 15 TTTTGGATTTTCTCCAGTTCAAGAACCAAGTGTGTGAGGAGCAGATGGAAG 74
QY 456 CATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGACTGGGTGAGCA 515
D 75 CATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGACTGGGTGAGCA 134
QY 516 TCTGCCAGCAGGAGACCTTCTGCTCTTTGACATTTGGAATAAACTTCAGCAATTTCCAGG 575
D 135 TCTGCCAGCAGGAGACCTTCTGCTCTTTGACATTTGGAATAAACTTCAGCAATTTCCAGG 194
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QY 576 AGCACCTGGATCTTCTCCAGCAGAGATAAAACAGAGAGTTTCCCTGACAGAAAGATG 635  
Db 195 AGCACCTGGATCTTCTCCAGCAGAGATAAAACAGAGAGTTTCCCTGACAGAAAGATG 254  
QY 636 AAATATCTGCAGAGAGACATTTGGAGAGCCTGGTGAACCAATTTGTCATTTCAACAGCAA 695  
Db 255 AAATATCTGCAGAGAGACATTTGGAGAGCCTGGTGAACCAATTTGTCATTTCAAC----- 309  
QY 696 TCTACATTTCAAGACTTGGCGAGTATTCTAAGAAACCCCTCAGAGAGCAAAATTCAGA 755  
Db 310 -----AGA 312  
QY 756 TGTGCGCAACGTCACCTTGGGCGCTTTCCCTCTCACTCCTGATGACACCCCTCTCTCAATGA 815  
Db 313 TGTGCGCAACGTCACCTTGGGCGCTTTCCCTCTCACTCCTGATGACACCCCTCTCTCAATGA 372  
QY 816 AATTTCTCGATTAATACATCAACGACACCAAGATGCCCTAACAGAAAGAGAAACAGAAAT 875  
Db 373 AATTTCTCGATTAATACATCAACGACACCAAGATGCCCTAACAGAAAGAGAAACAGAAAT 432  
QY 876 CGCTGTGTGGAGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGGTAAACAGAGATTCAA 935  
Db 433 CGCTGTGTGGAGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGGTAAACAGAGATTCAA 492  
QY 936 GGCAGAGCTCGCTGACTCCAGTCCCATATTTACAGAGCTAGCAGGAAGTCCCAACT 995  
Db 493 GGCAGAGCTCGCTGACTCCAGTCCCATATTTACAGAGCTAGCAGGAAGTCCCAACT 552  
QY 996 TCAGATGCAAAAGATATTTAAGAACTCCAGGATTCAGAAATCCATGTGTAGGAT 1055  
Db 553 TCAGATGCAAAAGATATTTAAGAACTCCAGGATTCAGAAATCCATGTGTAGGAT 612  
QY 1056 TAGACCAAGAAAGAAAGATGCTCAAGCTCCACAGAGATCAACTTACGGCCATCTT 1115  
Db 613 TAGACCAAGAAAGAAAGATGCTCAAGCTCCACAGAGATCAACTTACGGCCATCTT 672  
QY 1116 TAAGAGACAGCTCAGAGCAAAAGCCCTGCAAGTGACCTCTCTCTTTGATTTCCAA 1175  
Db 673 TAAGAGACAGCTCAGAGCAAAAGCCCTGCAAGTGACCTCTCTCTTTGATTTCCAA 732  
QY 1176 CAAAAATTTGAAAGTGAAGAGTCTATCATGGAACCATGGAGGAGCAAGCAACCAAGAAAT 1235  
Db 733 CAAAAATTTGAAAGTGAAGAGTCTATCATGGAACCATGGAGGAGCAAGCAACCAAGAAAT 792  
QY 1236 CTATCTCAGAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCATAGAGAGAAACAATC 1295  
Db 793 CTATCTCAGAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCATAGAGAGAAACAATC 852  
QY 1296 TTTGGATGTGGGACAAATTCAGTTCACTGATGAATTTGCTGGATCACTGCGACGCTTTGG 1355  
Db 853 TTTGGATGTGGGACAAATTCAGTTCACTGATGAATTTGCTGGATCACTGCGACGCTTTGG 912  
QY 1356 TCCTGACACCCAAATCAGAGCTGCCACATCTTTTGTGTTTATAACAGAGATGCTACTTT 1415  
Db 913 TCCTGACACCCAAATCAGAGCTGCCACATCTTTTGTGTTTATAACAGAGATGCTACTTT 972  
QY 1416 GAGTCCAGAACTTCTCTGTTGAACCCAGCTTTGAGACAGTGGAGCGAGCAGCATGG 1475  
Db 973 GAGTCCAGAACTTCTCTGTTGAACCCAGCTTTGAGACAGTGGAGCGAGCAGCATGG 1032  
QY 1476 TCTACCTGACACTTTTGGTCTCCACTGCTATGGCTCTACCTCCCTGTGAGAGCTCC 1535  
Db 1033 TCTACCTGACACTTTTGGTCTCCACTGCTATGGCTCTACCTCCCTGTGAGAGCTCC 1092  
QY 1536 ACCTTTCTTTATGGCATCAAGCATCTTCTCTGATCTGATCAGGACCCACAGATACAAAT 1595  
Db 1093 ACCTTTCTTTATGGCATCAAGCATCTTCTCTGATCTGATCAGGACCCACAGATACAAAT 1152  
QY 1596 GGCCACTGACAGCAATGTAGTACAGGGGCTCACCATCCCAACAGATGATTTCTGC 1655  
Db 1153 GGCCACTGACAGCAATGTAGTACAGGGGCTCACCATCCCAACAGATGATTTCTGC 1212  
QY 1656 AATCAGCCAACTGGCTCTGGGAATTTCAATCCACTGCAATCTTCAGATGACAGCGGATC 1715

Db 1213 AATCAGCCAACTGGCTCTGGGAATTTTCATCCACCTGCATCTTCAGATGACAGCGGATC 1272  
QY 1716 AAGTGCAGGTGGCGAAGATATGGTCAGACACCTAGATGAATTTGATCTGTCTGACACTCC 1775  
Db 1273 AAGTGCAGGTGGCGAAGATATGGTCAGACACCTAGATGAATTTGATCTGTCTGACACTCC 1332  
QY 1776 TGCCCCATCTGAGGTACACAGAGCTCAGCGAATATGTTTCTGTCCAGATCAATTTCTTGA 1835  
Db 1333 TGCCCCATCTGAGGTACACAGAGCTCAGCGAATATGTTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GGATACCACTCTCTGCTCAGCTTTTACAGTATATACCACTAGTTCTATAGACCAATGGCCCC 1895  
Db 1393 GGATACCACTCTCTGCTCAGCTTTTACAGTATATACCACTAGTTCTATAGACCAATGGCCCC 1452  
QY 1896 GAAGGGCCGAGAGCTGTGTAGTGTCTTTCAGTCTCGGTCTTCTAACATGGCTTCTCCAA 1955  
Db 1453 GAAGGGCCGAGAGCTGTGTAGTGTCTTTCAGTCTCGGTCTTCTAACATGGCTTCTCCAA 1512  
QY 1956 CGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTTCAACAGCT 2015  
Db 1513 CGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTTCAACAGCT 1572  
QY 2016 GCTGTTTCCATATCTPAAGATCCAAATCTTACAGGATTTTAAAGCAACTTGAATTAACCTT 2075  
Db 1573 GCTGTTTCCATATCTTACGATCCAAATCTTACAGGATTTTAAAGCAACTTGAATTAACCTT 1632  
QY 2076 CAGAAACGGGAGTGTGATTTGAATAGCAAAATGAACTTGAAGTCTGTGCGGTATAA 2135  
Db 1633 CAGAAACGGGAGTGTGATTTGAATAGCAAAATGAACTTGAAGTCTGTGCGGTATAA 1692  
QY 2136 CUTCACCAAGGCTGTGCACGGGGTCTTGGAGGATTTTCTGTTCTGCTGAGGCCCAACACT 2195  
Db 1693 CUTCACCAAGGCTGTGCACGGGGTCTTGGAGGATTTTCTGTTCTGCTGAGGCCCAACACT 1752  
QY 2196 CCATCTGGAATFAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAGAGATCCCTG 2255  
Db 1753 CCATCTGGAATFAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAGAGATCCCTG 1812  
QY 2256 CAAAGTTCCTGCGCTGCGCGGAATTTGGCCAAATGTTAAAGAAACGAACTGAGGAGAC 2315  
Db 1813 CAAAGTTCCTGCGCTGCGCGGAATTTGGCCAAATGTTAAAGAAACGAACTGAGGAGAC 1872  
QY 2316 GGAGTGTCTGTGCAAAACAGGATATGACAGCCAGGGAGCTTGAACGGTCTGGAACCGAG 2375  
Db 1873 GGAGTGTCTGTGCAAAACAGGATATGACAGCCAGGGAGCTTGAACGGTCTGGAACCGAG 1932  
QY 2376 CCTCTGTGGCCCTGGCAAAAAGGAATCGAGGTCTTCCAGGAAAGGAGCTCCATGCGAG 2435  
Db 1933 CCTCTGTGGCCCTGGCAAAAAGGAATCGAGGTCTTCCAGGAAAGGAGCTCCATGCGAG 1992  
QY 2436 GTTGCAGATCACTCTGAAAATCAAGCATACAAAACCTAGTGTAAAAAGTTTCCAAAATCA 2495  
Db 1993 GTTGCAGATCACTCTGAAAATCAAGCATACAAAACCTAGTGTAAAAAGTTTCCAAAATCA 2052  
QY 2496 ACAAAATTAACAGGATATCAGTAAAGAAATTTCTGAATTTACTGACCGTAGAATAGAGA 2555  
Db 2053 ACAAAATTAACAGGATATCAGTAAAGAAATTTCTGAATTTACTGACCGTAGAATAGAGA 2112  
QY 2556 ATTTAACCATCAAGATTTGGGAAGGAAATTTAAAACTGAAAATTTGTAATTTATCACTTAGG 2615  
Db 2113 ATTTAACCATCAAGATTTGGGAAGGAAATTTAAAACTGAAAATTTGTAATTTATCACTTAGG 2172  
QY 2616 CTATCTCAGAGAGATGATTTGCTTCTCAAGGAAATTTGAGAGAGGAGCATATTCATCGGT 2675  
Db 2173 CTATCTCAGAGAGATGATTTGCTTCTCAAGGAAATTTGAGAGAGGAGCATATTCATCGGT 2232  
QY 2676 CATCAAAATCCAGACATACAGTCAACACTGAGATCAGCAGACACCATATTTCAAAATATA 2735  
Db 2233 CATCAAAATCCAGACATACAGTCAACACTGAGATCAGCAGACACCATATTTCAAAATATA 2292  
QY 2736 GAAGAGTCATGTTCTTGGCAACGATAAATTTGAAAAAAGAACCTTACTTATTATTA 2795









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Db 2769 GTTCAGATACATACCATGGAATACTTACTTTCTGTGTACTACACAAAGCTATTTT 2828
QY 3276 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATACATAATCAAT 3330
Db 2829 AAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATACATAATCAAT 2883

RESULT 9
AAA46329
ID AAA46329 standard; DNA; 2244 BP.
XX
AC AAA46329;
XX
XX
DT 04-SEP-2000 (first entry)
XX
DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome 6q13-q15; ocular disease; retinal detachment;
KW choriorretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW rod- cone dystrophy; cone-rod dystrophy; ss.
XX
OS Homo sapiens.
XX
XX WO200026367-A2.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025440.
XX
XX 29-OCT-1998; 98US-00183972.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2000-365616/31.
XX
XX
XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
XX preventing, diagnosing and treating ocular disorders such as retinal
XX detachment and chorioretinal degeneration.
XX
XX Claim 3; Fig 19; 183pp; English.
XX
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an
XX additional intron after exon 5. The protein is an IPM component (IPMC).
XX Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX is located on chromosome 6q13-q15, between markers CHLC.GAT11P10 and
XX D6S284. The IPM proteins may be used to supplement a patient's own
XX production of the protein or to rectify alterations in their nucleic
XX acids that result in expression of an inactive protein. The IPM nucleic
XX acids may be used in this way to treat ocular diseases such as retinal
XX detachment, choriorretinal degeneration, retinal degeneration, age related
XX macular degeneration, photoreceptor degeneration, mucopolysaccharidosis, rod-
XX epithelium degeneration, cone degeneration, KPE (retinal pigment
XX cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX also be used to assay for other modulators of IPM proteoglycan expression
XX and activity that may be used to treat ocular diseases. The nucleic acids
XX and proteins may also be used as diagnostic reagents to detect the
XX presence of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
XX
XX
XX SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX
XX Query Match 65.6%; Score 2184.2; DB 3; Length 2244;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
XX
XX 1 TAAACCAAGAGGTTATCCTCAATCATCTGGTATCAATATATATATTTTTCACATTTC 60

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Db 22 TAAACCAAGAGGTTATCCTCAATCATCTGGTATCAATATATATTTTTCACATTTC 81
QY 61 TGTACTTTTAAATGAGATTTGAGGTTGTTCTGTGATTTGTTATCAGAATTACCAATGCAC 120
Db 82 TGTACTTTTAAATGAGATTTGAGGTTG-TCTGTGATTTGTTATCAGAATTACCAATGCAC 140
QY 121 AAAAGCCAGAATGTATTTTGGAACTAGAGAGCTATTTTGTGTTTTCGGATTTTCTCCA 180
Db 141 AAAAGCCAGAATGTATTTTGGAACTAGAGAGCTATTTTGTGTTTTCGGATTTTCTCCA 200
QY 181 AGTTCAAGGACCAACCAAGATATCTCAATTAAATATATATCAATCTGAAACTAAAGACATAGA 240
Db 201 AGTTCAAGGACCAACCAAGATATCTCAATTAAATATATATCAATCTGAAACTAAAGACATAGA 260
QY 241 CAATCCCCCAAGAAATGAACAACTGAAAGTACTGAAATAATGTACAAAATGTCAACTAT 300
Db 261 CAATNCCCACCAAGAAATGAACAACTGAAAGTACTGAAATAATGTACAAAATGTCAACTAT 320
QY 301 GAGACGAATATTCGATTTGGCAAGCATCGAACAAAAGATCCCGATTTTCCCAACGGG 360
Db 321 GAGACGAATATTCGATTTGGCAAGCATCGAACAAAAGATCCCGATTTTCCCAACGGG 380
QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTA 420
Db 381 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTA 440
QY 421 TAGATTGAGAGTGTGTCAGGAAGCAGTATGGAAAGCATATCGGATCTTTCTGGATCGCAT 480
Db 441 TAGATTGAGAGTGTGTCAGGAAGCAGTATGGAAAGCATATCGGATCTTTCTGGATCGCAT 500
QY 481 CCCTGACACAGGGGAATATCAGGACTGCGTCAGCATCTGCCAGCAGGAGAGACCTTCTGCCT 540
Db 501 CCCTGACACAGGGGAATATCAGGACTGCGTCAGCATCTGCCAGCAGGAGAGACCTTCTGCCT 560
QY 541 CTTTGACATTGGAAAAAATCTTCAGCAATTCCTCAGGAGCAGCTCGATCTTCTCCAGCAGAG 600
Db 561 CTTTGACATTGGAAAAAATCTTCAGCAATTCCTCAGGAGCAGCTCGATCTTCTCCAGCAGAG 620
QY 601 AATAAACACAGAGAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAGACATTTGGG 660
Db 621 AATAAACACAGAGAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAGACATTTGGG 680
QY 661 AGAGCCTGTGTGAAACCATTTCTCATTTCAACAGCAATCTACATTTCAAGAGCTTTGGGCGT 720
Db 681 AGAGCCTGTGTGAAACCATTTCTCATTTCAACAGCAATCTACATTTCAAGAGCTTTGGGCGT 740
QY 721 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAACGCTCTCACTTGGGCGCT 780
Db 741 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAACGCTCTCACTTGGGCGCT 800
QY 781 TTCCTCTCACTCTCTGATGACACCCCTCCTCAATGAATTTCTGATATACACTCAACGAC 840
Db 801 TTCCTCTCACTCTCTGATGACACCCCTCCTCAATGAATTTCTGATATACACTCAACGAC 860
QY 841 ACCAAGATGCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 861 ACCAAGATGCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
QY 901 GAGCTCAGGCTCTCTCTGTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 921 GAGCTCAGGCTCTCTCTGTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
QY 961 CCATATTACAGGAGCTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 981 CCATATTACAGGAGCTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
QY 1021 CTTCCAGGATTCAGAAAAATTCATGTTAGGATTTAGCAAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1041 CTTCCAGGATTCAGAAAAATTCATGTTAGGATTTAGCAAGAGAGAGAGAGAGAGAGAGAG 1100
QY 1081 TCAAGCTCCACAGAGATGCAATTTAGGGCCATCTTTAAGAGACACAGTGCAGAGCAAAA 1140

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Db 1101 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAACAAA 1160  
QY 1141 AGCCCTGCAAGTGAAGTCTCTCTGCTTTTATTCACACAAATTTGAAAGTGAAGAGTCTAT 1200  
Db 1161 AGCCCTGCAAGTGAAGTCTCTCTGCTTTTATTCACACAAATTTGAAAGTGAAGAGTCTAT 1220  
QY 1201 CATGGAACATGAGAGAGAGCAAGCAACAGAAATCTATCTCACAGCTACAGACCTCAAA 1260  
Db 1221 CATGGAACATGAGAGAGAGCAAGCAACAGAAATCTATCTCACAGCTACAGACCTCAAA 1280  
QY 1261 AGGCTGATCAGCAAGACTAGAGAGAGCAAGCAACATTTTGGATGAGGAGCAATTCAGTTC 1320  
Db 1281 AGGCTGATCAGCAAGACTAGAGAGAGCAAGCAACATTTTGGATGAGGAGCAATTCAGTTC 1340  
QY 1321 ACTGATGAATTTGCTGATCACTGCGAGCCTTTGGTCTGACACCCCAATCAGAGCTGCC 1380  
Db 1341 ACTGATGAATTTGCTGATCACTGCGAGCCTTTGGTCTGACACCCCAATCAGAGCTGCC 1400  
QY 1381 ACATCTTTTGTGTTATTAACAGAGAGTCTACTTTGAGTCAGAACTTCCTCTCGTTGAA 1440  
Db 1401 ACATCTTTTGTGTTATTAACAGAGAGTCTACTTTGAGTCAGAACTTCCTCTCGTTGAA 1460  
QY 1441 CCCAGCTTGACAGAGTGGAGCGGACGAGAGCATGCTTACCTGACACTTCTTGTCTCCA 1500  
Db 1461 CCCAGCTTGACAGAGTGGAGCGGACGAGAGCATGCTTACCTGACACTTCTTGTCTCCA 1520  
QY 1501 CCTGCTATGGCTCTACTCTCTCTGTCAGAGCTCCACTTTTATTTGAGCATCAAGCATC 1560  
Db 1521 CCTGCTATGGCC-CTACTCTCTCTGTCAGAGCTCCACTTTTATTTGAGCATCAAGCATC 1579  
QY 1561 TTCTCTCTGATGATCAAGGACACACAGATCAATGCGCCACTGACAGCAATGCTAGTA 1620  
Db 1580 TTCTCTCTGATGATCAAGGACACACAGATCAATGCGCCACTGACAGCAATGCTAGTA 1639  
QY 1621 CCAGGCTCACATCCACACAGTATTTATTCGAATCAGCCAACTGGCTCTGGGAAT 1680  
Db 1640 CCAGGCTCACATCCACACAGTATTTATTCGAATCAGCCAACTGGCTCTGGGAAT 1699  
QY 1681 TCACATCCACTGATCTTCAATGACAGCGGATCAAGTCAGAGTGGCGAAGATATGGTC 1740  
Db 1700 TCACATCCACTGATCTTCAATGACAGCGGATCAAGTCAGAGTGGCGAAGATATGGAC 1759  
QY 1741 AGACACCTAGATGAATGGATCTGTCGACACTCTGCCCCATCTGAGGTACAGAGCTC 1800  
Db 1760 AGACACCTAGATGAATGGATCTGTCGACACTCTGCCCCATCTGAGGTACAGAGCTC 1819  
QY 1801 AGCGAATATGTTCTGTCAGATCAATCTTGGAGATACCACTCTGTCAGCTTTA 1860  
Db 1820 AGCGAATATGTTCTGTCAGATCAATCTTGGAGATACCACTCTGTCAGCTTTA 1879  
QY 1861 CAGTATATCACCACTAGTCTTATGACCATTTGCCCAAGGCGGAGAGCTGGTAGTTC 1920  
Db 1880 CAGTATATCACCACTAGTCTTATGACCATTTGCCCAAGGCGGAGAGCTGGTAGTTC 1939  
QY 1921 TTGAGTGGGTGTGTATACATGGGCTTCTCAAGACTGTTTCAACAGAGCTCTCTG 1980  
Db 1940 TTGAGTGGGTGTGTATACATGGGCTTCTCAAGACTGTTTCAACAGAGCTATTTG 1999  
QY 1981 GAGTACCGAGCTCTGGAGCAACATTCACACAGCTGCTGGTTCATCTACGATCCAT 2040  
Db 2000 GAGTACCGAGCTCTGGAGCAACATTCACACAGCTGCTGGTTCATCTACGATCCAT 2059  
QY 2041 CTTACAGGATTTAAGCAACTTGAATCTTAACTTCAGAAACGGGAGTGTGATTTGAAT 2100  
Db 2060 CTTACAGGATTTAAGCAACTTGAATCTTAACTTCAGAAACGGGAGTGTGATTTGAAT 2119  
QY 2101 AGCAAAATGAATTTCTAGTCTGCGGTATTAACCTCACCAGGCTGTGACGGGTC 2160  
Db 2120 AGCAAAATGAATTTCTAGTCTGCGGTATTAACCTCACCAGGCTGTGACGGGTC 2179  
QY 2161 TTGAGGATTTTCTGTTCTGTCAGGCGCCCAACTCTCGAAATAGACAGTACTCT 2220  
Db 2180 TTGAGGATTTTCTGTTCTGTCAGGCGCCCAACTCTCGAAATAGACAGTACTCT 2239

QY 2221 CTC 2223  
Db 2240 CTC 2242

## RESULT 10

ADAL4844

ID ADAL4844 standard; cDNA; 2244 BP.

XX AC ADAL4844;

XX DT 06-NOV-2003 (first entry)

XX XX Human interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.

DE ss; gene; human; IPMC 150 isoform C; gene therapy;

XX interphotoreceptor matrix component; IPMC; ocular disorder;

KW macular degeneration; photoreceptor death; retinal detachment.

XX OS Homo sapiens.

XX FH Key

FT CDS

FT Location/Qualifiers

FT 151..747

FT /tag= b

FT /product= "IPMC 150 isoform C"

FT sig\_peptide

FT 151..200

FT /tag= a

FT /note= "Signal sequence"

FT mat\_peptide

FT 201..744

FT /tag= c

FT /note= "Mature IPMC 150 isoform C"

FT 265..267

FT /tag= d

FT /note= "Encodes Pro"

FT unsure

FT 346..348

FT /tag= e

FT /note= "Encodes His"

FT XX

PN US2002160954-A1.

XX 31-OCT-2002.

XX 08-NOV-2001; 2001US-00007270.

XX 29-OCT-1998; 99US-00183972.

XX 29-OCT-1999; 99US-00430195.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2003-238235/23.

XX P-PSDB; ADAL4845.

XX New isolated or recombinant interphotoreceptor matrix component

XX polynucleotide and polypeptide, useful for diagnosing, preventing,

XX treating or prognosticating ocular disorders, e.g. macular degeneration

XX or retinal detachment.

XX Claim 3; Page 36-37; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor

XX matrix component (IPMC) polynucleotide. Also disclosed is a vector

XX comprising a promoter of an interphotoreceptor matrix component (IPMC)

XX gene operatively linked to the IPMC polynucleotide. The IPMC

XX polynucleotides, polypeptides and antibodies are useful for diagnosing,

XX preventing, treating or prognosticating ocular disorders, e.g. macular

XX degeneration, photoreceptor death or retinal detachment. They are also

XX useful for identifying a compound capable of modulating IPMC gene

XX expression in a cell. The present sequence represents cDNA encoding human

XX interphotoreceptor matrix component, IPMC, 150 isoform C.

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SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;									
Query Match 65.6%; Score 2184.2; DB 7; Length 2244;									
Best Local Similarity 99.5%; Pred. No. 0;									
Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2									
QY	1	TAAACCAAGAAGGTATCTCTCAATCATCTGGTATCAATATATAATATATTTTTCACATTTC	60						
DB	22	TAAACCAAGAAGGTATCTCTCAATCATCTGGTATCAATATATAATATATTTTTCACATTTC	81						
QY	61	TGTTACTTTTTTAATGAGATTTCAGGTGTCTCTGTGATCTGTATCAGAAATTCACATGCAC	120						
DB	82	TGTTACTTTTTTAATGAGATTTCAGGTGTCTCTGTGATCTGTATCAGAAATTCACATGCAC	140						
QY	121	AAAAGCCAGAAATGTTATTTGGAACATAGAAAGAGCTATTTTTTGTGATTTTTCTCCA	180						
DB	141	AAAAGCCAGAAATGTTATTTGGAACATAGAAAGAGCTATTTTTTGTGATTTTTCTCCA	200						
QY	181	AGTTCAAGGAACCAAGAGATATCTCCATTAAACATATACCAATCTCGAACTTAAAGACATAGA	240						
DB	201	AGTTCAAGGAACCAAGAGATATCTCCATTAAACATATACCAATCTCGAACTTAAAGACATAGA	260						
QY	241	CAATCCCCCAAGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTAT	300						
DB	261	CAATNCCCACAGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTAT	320						
QY	301	GAGACGAATATTCGATTTTGGCAAGCAGTCGAACAAAGATCCGCATTTTCCCAACGGG	360						
DB	321	GAGACGAATATTCGATTTTGGCAAGCAGTCGAACAAAGATCCGCATTTTCCCAACGGG	380						
QY	361	GGTTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTA	420						
DB	381	GGTTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTA	440						
QY	421	TAGATTGAGAGTGTCTCAGGAAGCAGTATGGAGAGCATATCGATCTTTTCTGGATCGCAT	480						
DB	441	TAGATTGAGAGTGTCTCAGGAAGCAGTATGGAGAGCATATCGATCTTTTCTGGATCGCAT	500						
QY	481	CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCAGCAGGAGAGCATCTTCGCCT	540						
DB	501	CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCAGCAGGAGAGCATCTTCGCCT	560						
QY	541	CTTTGACATTGGAAGAAACTTCAGCAATTTCCAGGAGCACTGATCTTCCAGCAGAG	600						
DB	561	CTTTGACATTGGAAGAAACTTCAGCAATTTCCAGGAGCACTGATCTTCCAGCAGAG	620						
QY	601	AATAAAACAGAGAAAGTTTCCCTGACAGAAAAGATGAAATATCTCGACAGAGAGCATTTGGG	660						
DB	621	AATAAAACAGAGAGTTTCCCTGACAGAAAAGATGAAATATCTCGACAGAGAGCATTTGGG	680						
QY	661	AGAGCCTGGTGAACACCATTTGTCATTTCAACAGCAATCTACATTTCAAGAGCTTGGGCAGT	720						
DB	681	AGAGCCTGGTGAACACCATTTGTCATTTCAACAGCAATCTACATTTCAAGAGCTTGGGCAGT	740						
QY	721	ATTTCTAAGAAAACCTTCAGAGAGCAATTTCAAGATGTTGCCACAGTCTCATTGGGCCT	780						
DB	741	ATTTCTAAGAAAACCTTCAGAGAGCAATTTCAAGATGTTGCCACAGTCTCATTGGGCCT	800						
QY	781	TTCCCTCTCACTCTGTATGACACCTCTCAATGAAATTTCTCGATAATACACTCAAGCAC	840						
DB	801	TTCCCTCTCACTCTGTATGACACCTCTCAATGAAATTTCTCGATAATACACTCAAGCAC	860						
QY	841	ACCAAGATGCTTACAAACAGAAAGAAACAGAAATTCGCTGTGTTGGAGGAGCAGAGGTG	900						
DB	861	ACCAAGATGCTTACAAACAGAAAGAAACAGAAATTCGCTGTGTTGGAGGAGCAGAGGTG	920						
QY	901	GAGCTCAGCGCTCTCTCTGTGTAAACCGAAGTTCGAAGTCAGAGTCTCGTCTACTCCAGTCC	960						
DB	921	GAGCTCAGCGCTCTCTCTGTGTAAACCGAAGTTCGAAGTCAGAGTCTCGTCTACTCCAGTCC	980						
QY	961	CCATATTACAGGAGCTAGCAGGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA	1020						
DB	981	CCATATTACAGGAGCTAGCAGGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA	1040						

QY 2101 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGGTATTAACCTCAACAGGCTGTGCACGGGTC 2160  
 DB 2120 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGGTATTAACCTCAACAGGCTGTGCACGGGTC 2179  
 QY 2161 TTGGAGGATTTTGGTCTGTGCGGCAACCAATCCATCTGGAATAGACAGTACTCT 2220  
 DB 2180 TTGGAGGATTTTGGTCTGTGCGGCAACCAATCCATCTGGAATAGACAGTACTCT 2239

QY 2221 CTC 2223  
 DB 2240 CTC 2242

RESULT 11  
 ID ACC57948  
 AC ACC57948 standard; cDNA; 2244 BP.

XX AC ACC57948;

DT 11-AUG-2003 (first entry)

XX Human interphotoreceptor matrix IPM 150, isoform C, cDNA.

XX Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
 receptor; ophthalmological; gene therapy; gene; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 151..747

FT /\*tag= a

FT /product= "IPM 150"

FT sig\_peptide 151..210

FT /\*tag= b

FT /\*tag= c

FT /\*note= "encodes Pro"

FT /\*tag= d

FT /\*note= "encodes His"

XX WO2003039346-A2.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036090.

XX 08-NOV-2001; 2001US-00077270.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2003-441440/41.

XX P-PSDB; ABR42344.

XX New interphotoreceptor matrix proteins and polynucleotides, useful for

XX treating or preventing photoreceptor death or retinal detachment, or for

XX treating ocular disorders.

XX Claim 1; Page 79-80; 105pb; English.

XX The present sequence is that of cDNA encoding isoform C of novel human  
 XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
 XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
 XX is located on chromosome 6q13-q15, a region that also contains loci for  
 XX progressive bifocal choriorretinal atrophy, autosomal dominant Stargardt's  
 XX -like macular dystrophy, North Carolina macular dystrophy and Salla  
 XX disease. Members of the IPMC gene family have been identified in humans,  
 XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
 XX Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or IPM2). The  
 XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
 XX antibodies that specifically bind the polypeptides, and vectors

CC comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
 CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression  
 XX

SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;

Query Match 65.6%; Score 2184.2; DB 8; Length 2444;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATAATATTTTTCACATTTC 60  
 DB 22 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATAATATTTTTCACATTTC 81  
 QY 61 TGTACTTTTAAATGAGATTTGAGTTCTTCTGTGATTTGTTATCAGAAATACCAATGAC 120  
 DB 82 TGTACTTTTAAATGAGATTTGAGTTCTTCTGTGATTTGTTATCAGAAATACCAATGAC 140  
 QY 121 AAAAGCCAGAAATGTTTGGAACTAGAGAGCATTTTCTGTTTTCGATTTCCTCA 180  
 DB 141 AAAAGCCAGAAATGTTTGGAACTAGAGAGCATTTTCTGTTTTCGATTTCCTCA 200  
 QY 181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTCTGAAACTAAAGACATAGA 240  
 DB 201 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTCTGAAACTAAAGACATAGA 260  
 QY 241 CAATCCCCCAAGAAATGAAACACTGAAAGTACTGAAAAATGTACAAAATGTCAACTAT 300  
 DB 261 CAATNCCCCCAAGAAATGAAACACTGAAAGTACTGAAAAATGTACAAAATGTCAACTAT 320  
 QY 301 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAAGATCCGCATTTTCCCAACGGG 360  
 DB 321 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAAGATCCGCATTTTCCCAACGGG 380  
 QY 361 GGTTAAAGTCTGTCCACAGGAATCGATGAACACAGATTTTAGACAGTCTTCAAGCTTATTA 420  
 DB 381 GGTTAAAGTCTGTCCACAGGAATCCATGAACACAGATTTTAGACAGTCTTCAAGCTTATTA 440  
 QY 421 TAGATTGAGAGTGTCTCAGGAAGCAGTATGGAAGCATATCGGATCTTCTCGGATCGCAT 480  
 DB 441 TAGATTGAGAGTGTCTCAGGAAGCAGTATGGAAGCATATCGGATCTTCTCGGATCGCAT 500  
 QY 481 CCCTGACACAGGGGAATATCAGGACTGGTCTCAGCATCTGCCAGCAGGAGACCTTCTGCCT 540  
 DB 501 CCCTGACACAGGGGAATATCAGGACTGGTCTCAGCATCTGCCAGCAGGAGACCTTCTGCCT 560  
 QY 541 CTTTGACATTGGAAAAAATCTCAGCAATTCCTCAGGAGCAGCTGGATCTTCTCCAGCAGAG 600  
 DB 561 CTTTGACATTGGAAAAAATCTCAGCAATTCCTCAGGAGCAGCTGGATCTTCTCCAGCAGAG 620  
 QY 601 AATAAACACAGAGAAGTTTCCCTGACAGAAAAAGATGAAATATCTCAGAGAGAAGACATTGGG 660  
 DB 621 AATAAACACAGAGAAGTTTCCCTGACAGAAAAAGATGAAATATCTCAGAGAGAAGACATTGGG 680  
 QY 661 AGAGCTGTGTAACCACTGTCTTCAATTCACAGCAATCTACATTTCAAGACTTGGGAGT 720  
 DB 681 AGAGCTGTGTAACCACTGTCTTCAATTCACAGCAATCTACATTTCAAGACTTGGGAGT 740  
 QY 721 ATTCTAAGAAAAACCTCAGAGAGACAAATTCAGATGTTCGCAACGCTCTCACTTTGGGCT 780  
 DB 741 ATTCTAAGAAAAACCTCAGAGAGACAAATTCAGATGTTCGCAACGCTCTCACTTTGGGCT 800  
 QY 781 TTCCCTCTCACTCTGTATGACACCTCTCAATGAAATTTCTCGAATAATACACTCAACGAC 840  
 DB 801 TTCCCTCTCACTCTGTATGACACCTCTCAATGAAATTTCTCGAATAATACACTCAACGAC 860  
 QY 841 ACCAGATGCTCAACACAGAAAGAAACCAATTCCTGTTGTTGGAGGAGCAGAGGTG 900  
 DB 861 ACCAGATGCTCAACACAGAAAGAAACCAATTCCTGTTGTTGGAGGAGCAGAGGTG 920  
 QY 901 GAGCTCAGCGTCTCTCTGTTAAACAGAAAGTTCAAGGCAGAGCTCGCTGACTCCAGTCC 960

Db 921 GAGCTCAGGCTCTCTCTGGTAAACAGAGAGTTCAAGGCAGAGCTCGCTGACTCCAGTCC 980  
QY 961 CCATATTACGAGGAGCTAGCAGGAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA 1020  
Db 981 CCATATTACGAGGAGCTAGCAGGAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA 1040  
QY 1021 CTTCCAGGATTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGC 1080  
Db 1041 CTTCCAGGATTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGC 1100  
QY 1081 TCAGCTCCACAGAGATGCAATCTTACGCCCAATTTAAGAGACACAGTGCAGAGCAAAA 1140  
Db 1101 TCAGCTCCACAGAGATGCAATCTTACGCCCAATTTAAGAGACACAGTGCAGAGCAAAA 1160  
QY 1141 AGCCTGCAAGTGACCTCTCTCTCTTTGATTCCAAACAAATTTGAAGTGGAGGAGTCTAT 1200  
Db 1161 AGCCTGCAAGTGACCTCTCTCTCTTTGATTCCAAACAAATTTGAAGTGGAGGAGTCTAT 1220  
QY 1201 CATGGAACCATGGAGGAGGACAAACCAAGAAATCTATCTCAGCTACAGACCTCAAA 1260  
Db 1221 CATGGAACCATGGAGGAGGACAAACCAAGAAATCTATCTCAGCTACAGACCTCAAA 1280  
QY 1261 AGGCTGATCAGCAAGCACTAGAGGAAGAACAAATCTTTGGATGTGGGACAAATTCAGTTC 1320  
Db 1281 AGGCTGATCAGCAAGCACTAGAGGAAGAACAAATCTTTGGATGTGGGACAAATTCAGTTC 1340  
QY 1321 ACTGATGAAATTTGCTGATCACTCCAGCTTTGGTCTCAGACCCCAATCAGAGCTGCC 1380  
Db 1341 ACTGATGAAATTTGCTGATCACTCCAGCTTTGGTCTCAGACCCCAATCAGAGCTGCC 1400  
QY 1381 ACATCTTTCTGTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTGAA 1440  
Db 1401 ACATCTTTCTGTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTGAA 1460  
QY 1441 CCCAGCTTCAGACAGTGGAGCGGACGACGATGCTCTACCTGACACATCTTGGTCTCCA 1500  
Db 1461 CCCAGCTTCAGACAGTGGAGCGGACGACGATGCTCTACCTGACACATCTTGGTCTCCA 1520  
QY 1501 CTTGCTATGGCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATC 1560  
Db 1521 CTTGCTATGGCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATC 1579  
QY 1561 TTCTCTGCTGATCAAGGACACACAGATACAAATGGGCACTGACAGACAAATGCTAGTA 1620  
Db 1580 TTCTCTGCTGATCAAGGACACACAGATACAAATGGGCACTGACAGACAAATGCTAGTA 1639  
QY 1621 CCAGGCTCACCATCCCAAGCTGATTTCTGCAATCAGCCCACTGGCTCTGGGAAT 1680  
Db 1640 CCAGGCTCACCATCCCAAGCTGATTTCTGCAATCAGCCCACTGGCTCTGGGAAT 1699  
QY 1681 TCACATCCAGCTGATCTTCCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATGGTC 1740  
Db 1700 TCACATCCAGCTGATCTTCCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATGGAC 1759  
QY 1741 AGACACTAGATGAATGATCTGCTGACATCTCCGCCCATCTCAGGTACAGAGTTC 1800  
Db 1760 AGACACTAGATGAATGATCTGCTGACATCTCCGCCCATCTCAGGTACAGAGTTC 1819  
QY 1801 AGCGAATATGTTCTCTCCAGATCAATTTCTGGAGGATACCACCTCTCTCAGCTTTA 1860  
Db 1820 AGCGAATATGTTCTCTCCAGATCAATTTCTGGAGGATACCACCTCTCTCAGCTTTA 1879  
QY 1861 CAGTATATCACCAGTATGTTCTATGACATGCCCCCAAGGCCGAGAGTGTAGTGTTC 1920  
Db 1880 CAGTATATCACCAGTATGTTCTATGACATGCCCCCAAGGCCGAGAGTGTAGTGTTC 1939  
QY 1921 TTCAGTCTGGTGTCTTAACTAGGCTTTCTCCACGACCTGTCTCAACAGAGCTCTCTG 1980  
Db 1940 TTCAGTCTGGTGTCTTAACTAGGCTTTCTCCACGACCTGTCTCAACAGAGCTATTTG 1999  
QY 1981 GAGTACCGAGCTGTGGAGCAAAATTCACAGAGCTGTGGTTCTCATATCTACGATCCAAAT 2040

Db 2000 GAGTACCGAGCTCTGGAGCAAAATTCACAGAGCTGTGGTTCCATATCTACGATCCAAAT 2059  
QY 2041 CTTACAGGATTTAAGCAACTTGAAATACTTAACCTTCAGAAAACGGAGTGTGATTGTGAAT 2100  
Db 2060 CTTACAGGATTTAAGCAACTTGAAATACTTAACCTTCAGAAAACGGAGTGTGATTGTGAAT 2119  
QY 2101 AGCAAAATGAAGTTTCTGAAGTCTGTGGGTATACCTTCAACAGGCTGTGCACGGGTC 2160  
Db 2120 AGCAAAATGAAGTTTCTGAAGTCAAGTGGGTATACCTTCAACAGGCTGTGCACGGGTC 2179  
QY 2161 TTGGAGGATTTTCTGTTCTGCTGACGCCCAACAACTCTCTGGAATAGACAGCTACTCT 2220  
Db 2180 TTGGAGGATTTTCTGTTCTGCTGACGCCCAACAACTCTCTGGAATAGACAGCTACTCT 2239  
QY 2221 CTC 2223  
Db 2240 CTC 2242

RESULT 12  
ADA14847  
ID ADA14847 standard; cDNA; 3668 BP.  
XX AC ADA14847;  
XX XX  
DT 06-NOV-2003 (first entry)  
XX Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.  
DE ss; gene; mouse; IPMC 150 isoform A; gene therapy;  
XX interphotoreceptor matrix component; IPMC; ocular disorder;  
KW macular degeneration; photoreceptor death; retinal detachment.  
KW  
XX Mus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 196..2592  
FT /\*tag= a  
FT /product= "IPMC 150 isoform A"  
XX  
XX US2002160954-A1.  
XX 31-OCT-2002.  
XX  
XX 08-NOV-2001; 2001US-00007270.  
XX  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX WPI; 2003-238235/23.  
XX P-PSDB; ADA14848.  
XX  
XX New isolated or recombinant interphotoreceptor matrix component polynucleotide and polypeptide, useful for diagnosing, preventing, treating or prognosticating ocular disorders, e.g. macular degeneration or retinal detachment.  
XX  
XX Claim 3; Page 39-41; 76pp; English.  
XX  
XX The invention relates to an isolated or recombinant interphotoreceptor matrix component (IPMC) polynucleotide. Also disclosed is a vector comprising a promoter of an interphotoreceptor matrix component (IPMC) gene operatively linked to the IPMC polynucleotide. The IPMC polynucleotides, polypeptides and antibodies are useful for diagnosing, preventing, treating or prognosticating ocular disorders, e.g. macular degeneration, photoreceptor death or retinal detachment. They are also useful for identifying a compound capable of modulating IPMC gene expression in a cell. The present sequence represents cDNA encoding mouse interphotoreceptor matrix component, IPMC, 150 isoform A.

XX	Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;	
SQ	Query Match Best Local Similarity 41.3%; Score 1375.6; DB 7; Length 3668; Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;	
QY	1 TAAACCAAGAGGTTATCTCTCAATCATCTGGTATCAATATATAATATTTTTCACATTTTC 60	954 GCTCACCRAACTCTGGGTACCACATCTACAGGAACCTGGTGGGACAGTCCCAACTCAGTT 1013
DB	62 TAAACCAAGGAGGTCGTCTGTACTCAGCCGACCTGGATTGATTATTTTCATATTTTC 121	1002 GCATAAGATATTTTAAAGAACTTCCAGGATTCATAAATAATCCATGTGTTAGGATTTAGACC 1061
QY	61 TGTACTTTTT-----AATGAGATTGAGTTGTTCTGTGATGTATCAGAAATPACC 113	1014 GCATAAGATATTTTAAAGAACTTCCAGGATTCGGAGAAATCCGTGTATTAGGATTTAGACC 1073
DB	122 AGTCACTTATTTCTTTAAGTGTGACTTGGTATTGTTCTGTGATTTT--TCAGAAATPACC 179	1062 AAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGGCATCTTTTAAAGAG 1121
QY	114 AATGCACAAAACCCAGAAATGATTTGAAACTAGAAAGCTATTTTGTGTTTTTGGATTT 173	1074 AAAGAAAGAAAGATGGTTCAAGCTCCACAGAAATACAGCTTATGGCCAATCTTAAAGAG 1133
DB	180 AGTATACAGAA--CCAGATGAATTTCAAATTAACATGCTATCTTTGTTTGGGATTT 238	1122 ACACAGTGCAGAAAGAAAGCCCTGCAAGTGAACCTCTCTGCTTTTGTGATTTCCAAATAAT 1181
QY	174 TTCTCCAAAGTTCAAGGAACCAAAGATATCTCCATTAACATATACCATCTGAAACTAAAG 233	1134 GGACCATGCAGAAAGAAAGCCCTGATAGTCACTACTGTCTCTGTGATTCACACAAAAT 1193
DB	239 TTCTCCAAAGTTCAAGGAATCAAGATACCTCTATTAAATATTCAGTCTCGAAATTAATA 298	1182 TGAAAGTGAAGGAGTCTATCTGGAACCATGGAGGACAGCAACACAGAAATCTATCT 1241
QY	234 ACATAGACAATCCCCCAAGAAATGAACAACATGAAAGTACTGAAAAATGTACAAATGT 293	1194 TGAAAGTGAAGAAATCCATCATGAGTCTATAGAA-----GACAAACACACAGAAACCTACT 1250
DB	299 ACATAGACAACCCCAAGAAATGAACAATTTGAAGTACTTCAAGTGCACAAAGTGT 358	1242 CACAGCTACAGACCTCAAAGGCTGATCAGCAAGCACTAGAGGAAGCAAACTTTTGA 1301
QY	294 CAACATGAGACGAATATTCGATTTGGCAAGCATCGAACAAAAGATCCGCAATTTTCC 353	1251 CACAGCTACAGACCTCAAAGAACTCATCATCAACTACTAGATGGAGACCTGTCTCTGGT 1310
DB	359 CAACATGAACGAATATTCGATTTGCCAAGCTTCGAACCAAAGATCAGCACTTTTCC 418	1302 TGTGGGACAAATTCAGTTTCACTGATGAATTTGCTGGATCACTGCCAGGCTTTTGTCTGTA 1361
QY	354 CAACGGGGTTAAAGTCTGTCCACAGAAATCCATGAACAGATTTTACAGTCTTCAAG 413	1311 AGAAGGGAATTTCCATTCGGTGAAGTACTGGGACACT-----CTTCAGACCTGT 1364
DB	419 CA----GCTGCTAAACATCTGTCCACAGGAATCTTTGACACAGATTTTAGCAAGTCTTCAAG 475	1362 CACCAATCAGAGCTGCCACATCTTTTGTCTGTTTATTAACAGAGGATGCTACTTTGAGTCC 1421
QY	414 CTTATTATAGATTGAGAGTGTGTGAGAAAGCAGTATGGGAAGCATATCGGATCTTTCTGG 473	1365 CACTGAACAGATCTGCCCAAGCCCTTGTCTGATGTACAGAGGATGCCACTTTGAGTCC 1424
DB	476 AATATTATAGACTGAGAGTATGTCAAGAGTCTGTGTTGGAGCATATCGTATCTTTCTGG 535	1422 AGAATCTCTCTGTTTGAACCCAGCTTGACAGAGTGGACGGAGGAGAGATGCTTACC 1481
QY	474 ATCCATCCCTGACACAGGGGAATATCAGGATGGGTGACATCTGCGACAGAGACCT 533	1425 AGAATCTCTCTGTTGAGCTTAGGCTTTAGGCACTGGACAGAGAGATCTGAGCTGCC 1484
DB	536 ACCGAATCTCTGACACAGAGGAATATCAAGACTGGGTGAGCCTCTGCGAAGAAACCT 595	1482 T-----GACACTTCTTGCTCTCCACCTGTCTATGCTGCTCTACTCTCCCTGTC 1526
QY	534 TCTGCTCTTTGACATTTGGAATAAATCTCAGCAATTCACAGGAGCCTGGATCTTCTCC 593	1485 TGGATGTCTCTCCAAAGACAGTTCTTGGTCTCCACCTGTATCAGGCTCAATTTCCCGATC 1544
DB	596 TCTGCTCTTTGACATTTGGGAATAAATCTCAGCAATTCACAGGAGCCTTAGATCTTCTTC 655	1527 AGAAGCTCAACTTTTATTTTATGGGATCAAGCATTTCTCTCTGATGATCAAGGACACAC 1586
QY	594 AGCAGAAATAAACAAGAGATTTCCCTGACAGAAAGATGAATATCTGCAGAGAAGA 653	1545 AGAAATCTAGCTTCGTTTCA---CACCTAGCATCTTCTCTAGATGCTCAAGGCCCTCC 1601
DB	656 AGCAGAAATAAACAAGAGATTTCCCTGGAGGAAGATGAGACAGCCTCCATGGAGA 715	1587 AGATACAAATGCGCACTGACACAGACAATGCTAGTACCAGGCTCACCATCCCCACCACTGA 1646
QY	654 CATTTGGAGAGCCTGGTGAACCATTTGCTATTTCAACAGCAATCTACATTTCAAGACTT 713	1602 TCCCTTGATGACCACTGGCCCAACAGCACTCATCCCAAGCCCACTCTCCCACTATGTA 1661
DB	716 CACTGGAAGCACCTTACTGGAAGCCCTGTGTATCCAC----- 752	1647 TTATTCTCAATCAGCCAACTGGCTCTGGGAATTTCACTCCACTGCTCATCTTCAGATGA 1706
QY	714 GGGCAGTATTCTAAGAAAAACCTCAGAAAGACAAATTCAGAGATGTTGCCAACTCTCACT 773	1662 TTATTCTACCATCCGCCAATTTGCCCTTGGAACTGTCACATTTGGCTGCTCATCTCCAGTGA 1721
DB	753 -----AGATGTTTCCAGGATGCTCCT 773	1707 CAGCCGATCAAGTGCAGGTGGCGAAGATATGGTCAGACACCTAGATGAATGGATCTGTC 1766
QY	774 TGGCCCTTTCCCTCTCACTCTGATGACACCTCTCTCAATGAATTTCTGATTAATACAT 833	1722 CAGAGAGTGTATCAAGCAGCCATGACAAATCCGAGACCTAGATGGCATGGATGTGTC 1781
DB	774 GGGCCCTTTCCCACTTCTCTGATGACAGACCTCAAGGAGATTTCTCAGTGTCACTCCT 833	1767 TCACACTCTCTCCCACTCTGAGGTACAGAGCTCAGCGAATATATTTCTGTCCCCAGATCA 1826
QY	834 CAACGACCAAGATGCTTCAACAGAAAGAGAAACAGAA-----TTCCGCTGT 881	1782 TCACAGCCCACTTGTTCAGAAATATCAGAACTCAGTGGATACGATTTCTGCTCGGTCA 1841
DB	834 CAAGCAATTTCAAAAGCCCAACAGAAAGTAAACAGAACTTATTCAGTGTCTGAAT 893	1827 TTTCTTGGAGATACCACTCTCTGCTCAGCTTTACAGTATATACCACTAGTTCTATGAC 1886
QY	882 GTTGGAGAGCAGAGGTGAGCTCAGCTCTCTCTGTTAAACAGAAAGTTCAAGGCAGA 941	1842 GTTCTTGGAGATGACCAACCCATCCCAAGTACAGTACGGTTTATCACCACCACTCCGAGAC 1901
DB	894 CTCATCAGAGAGAGGTGAATTCAGCATCTCTCTGCCAAACCAACAGGTTCAAGGCAGA 953	1887 CATTTGCCCCCAAGGGCGAGAGCTGTGTCTTCCAGTCTGCTGTCTGTAACATGGC 1946
QY	942 GCTCGCTGACTCCCACTATTTACCAAGGAGCTAGAGGAAGTCCCACTTCAGAT 1001	1902 CATTTGCCCAAGGGCAGAGCTAGTGGTATTTCTCAGGCTGGGTGTTGTTAACTATGCC 1961
		1947 CTTCTCCAAAGCACTGTTTCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATT 2006
		1962 GTTCTCTTATGACCTGTTCAAGAGTCTCTTGGAGTATCAAGCCCTGGAAACAACGATT 2021
		2007 CACAGACTGCTGTTCCATATCTACGATCCAATCTTACAGGATTTAAGCAACTTGAAT 2066
		2022 CACAGACTGCTGTTCTCTATCTACGATCGAATCTTTACGGGATTTAAGCAACTGGAAT 2081





QY 234 ACATAGACAATCCCCAAGAAATGAAACAACTGAAGTACTGAAAAATGTAACAAATGT 293  
DB 299 ACATAGACAAACCCCAAGATCGAACAATGAAAGTACTTCAACAGTGCACAAAGTGT 358  
QY 294 CAACTATGAGAGCAATATTCGATTTGGCAAGCAATGCAACAAAGATTCGCAATTTTCC 353  
DB 359 CAACCATGAAGCAATATTCGATTTGCCAAAGCTTCGAACCAAAAGATCAGCACTTTTCC 418  
QY 354 CAAAGGGGTTAAAGTCTGTCCACAGGAATCCATGAACACAGATTTAGACAGTCTTCAAG 413  
DB 419 CA---GCTGCTAAACATCTGTCCACAGGAATCCTTGAGACAGATTTAGCAAGTCTTCAAG 475  
QY 414 CTTATTAATAGATGAGAGTGTGTGAGGAAGCAATGAGGAAGCAATATCGGATCTTTCTGG 473  
DB 476 AATATTATAGACTGAGAGTATGTCAAGAAAGTGTGTGGGAAGCATATCGTATCTTTCTGG 535  
QY 474 ATCGCATCCCTGACACAGGGAATATCAGGATCGGTCCAGCATCTGCCAGCAGGACCT 533  
DB 536 ACCGAACTTCTGACACAGGAATATCAAGACTGGGTGAGCTCTGCCAGAAAGAACCT 595  
QY 534 TCTGCTCTTTGACATTTGGAAGAACTTTCAGCAATTTCCAGGAGCACTCGATCTTCTCC 593  
DB 596 TCTGCTCTTTGACATTTGGAAGAACTTTCAGCAACTCCAGGAGCACTTAGATCTTCTTC 655  
QY 594 AGCAGAGATTAACACAGAGAGTTCCTGACAGAAAGATGAAATATCTGCGAGAGA 653  
DB 656 AGCAGAGATTAACACAGAGAGTTCCTGCGAGAAAGATGACAGACCTCCATGAGAGA 715  
QY 654 CATTGGAGAGCCTGGTGAACCACTTGTCAATTTCAACAGCAATCTACATTTCAAAGACTT 713  
DB 716 CACTGGAAGCACTTACTGAGCCCTGTGTGTTACCAC----- 752  
QY 714 GGGCAGTATTTCAAGAAACCCCTCAGAAAGACAAATTCAGAGTGTGGCCAACTCTCACT 773  
DB 753 -----AGATGTTTCCAGGATGTCCCT 773  
QY 774 TGGGCTTTCCCTCTCACTCTGATGACCCCTCCTCAATGAAATTCCTGATTAATCACT 833  
DB 774 GGGGCTTTCCCACTTCTCTGATGACAGACCTCAAGAGATTTCTAGTGTACCCT 833  
QY 834 CAACGACACCAAGATGCTCAACAGAAAGAGAAACAGAA-----TTCGCTGT 881  
DB 834 CAAGGACATTCAAAGGCCCAACACAGAAAGTAAACAGAACTATTCACTGTCTGAAAT 893  
QY 882 GTTGGAGAGCAGAGGTGGAGCTCAGGCTCTCTCTGTTAAACAGAACTTCAAGCAGA 941  
DB 894 CTCATCAGAGAGAGGTGGAATTCAGCATCTCTCTGCCAAACCAAGTTCAGGCGAGA 953  
QY 942 GCTGCTGACTCCAGTCCCAATATTACAGGAGCTAGCAGGAAAGTCCCACTTCAGAT 1001  
DB 954 GCTCACCACCTCTGGGTCAACATACTACAGGAACTGGTGGGACAGTCCCACTGCAGTT 1013  
QY 1002 GCAAGATATTTAAGAACTTCAGGATTCAGAAATCCATGTGTAGGATTTAGACC 1061  
DB 1014 GCAAGATATTTAAGAACTTCAGGATTCAGGAAATCCGTGTATTAGGATTTAGACC 1073  
QY 1062 AAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGSCCATCTTTAAGAG 1121  
DB 1074 AAAGAAAGAGAGATGGTTCAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAG 1133  
QY 1122 ACAGGTGCGAGAGCAAAAGCCCTGCAAGTACCTCTCTCTTTGATTTCCAAACAAAT 1181  
DB 1134 GGACCATGCGAGAGCAAAAGCCCTGATAGTCTACTGTCTCTTGATTTCCAAACAAAT 1193  
QY 1182 TGAAGTGAAGAGTCTATCATGAAACCATGGAGGAGCAAGCAACCAAGATCTATCT 1241  
DB 1194 TGAAGTGAAGAGTCTCATCATGAGTCTAGAA---GACAAACACCAAGAACTTACCT 1250  
QY 1242 CACAGCTACAGACTCAAAAGCTGATCAGCAAGCACTAGAGAGAAAGCAATCTTTGGA 1301  
DB 1251 CACAGCTACAGACTCAAAAGCTGATCATCATCACTACTAGATGGAGACCTGTCTTGT 1310

QY 1302 TGTGGGCAAAATTCAGTTCACTGATGAATTCCTGATCACTGCCAGCCTTTGGTCTTGA 1361  
DB 1311 AGAAGGGAATAATTCATTCGGTGAATGAAGTACTTGGGACACT-----CTTCAGACCTGT 1364  
QY 1362 CACCAATCAGAGCTGCCACATCTTTTCTGTGTATAACAGAGGATGCTACTTTTCACTCC 1421  
DB 1365 CACTGAACAGATCTGCCAAGCCCTTGTGTATGTCAACAGAGGATGCCACTTTTCACTCC 1424  
QY 1422 AGAATTTCTCTCTGTGTGAACCCCACTTTGAGACATGTGAGACGGAGCAGATGTCTTACC 1481  
DB 1425 AGAATCTCTCTTGTGTGAGCCTTAGCCTTGAAGCAGTGAAGAGGATCTGAGCTGCC 1484  
QY 1482 T-----GACACTTCTTGTGTCTCCACTCTGATGGCTCTACTCTCTCTGTCC 1526  
DB 1485 TGGAAATGCTCTCAAGACAGTTCCTTGTCTCCACTGTATCAGCCTCAATTTCCCGATC 1544  
QY 1527 AGAAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTGTGATGATCAAGGACCAAC 1586  
DB 1545 AGAAAACTTACCTTCTGTTTA---CACCTAGCATCTTCTCTAGATGCTCAAGGCCCTCC 1601  
QY 1587 AGATACAAATGGCACTGACACAGACAACTAGTAGTACAGGGCTCACATCCCCACCACTGA 1646  
DB 1602 TCCCTTGTGACCACTGGCCCAACAGCACTCATCCCCAAGCCCACTTCCCACTATCGA 1661  
QY 1647 TTATTTCTCAATCAGCAACTGGCTCTGGGAATTTACATCCACTGCACTCTTTCAGATGA 1706  
DB 1662 TTATTTCTCACTCCGCAATTTGCTCTGGAATCGTCACTTGGGCTGCTCATCTCCAGTGA 1721  
QY 1707 CAGCCGATCAAGTGCAGGTGGGAGATATGGTCAGACACCTAGATGAATGGAATGATCTTC 1766  
DB 1722 CAGAGAGTGTATCAACAGACCATGACAAATCCGAGACCTAGATGGCATGGATGTCTC 1781  
QY 1767 TGACACTCTCTCCCACTTGAGGTACAGAGCTCAGCGAATATGTTCTGTCTCCAGATCA 1826  
DB 1782 TGACACGCGACCTTGTGAGAAATATCAGAACTCAGTGTGATACGATTCTGCTCGGGTCA 1841  
QY 1827 TTTCTTGAGAGATACCACTCTCTGCTCAGCTTACAGTATATCACCAGTATCTATGAC 1886  
DB 1842 GTTCTTGAGAGATGACCACACCCATCCCAACAGTACGGTTTATCACCACAGCTCCGAGAC 1901  
QY 1887 CATTGCCCCCAAGGCCGAGAGCTGGTAGTGTCTTCTCAGTCTGGGTGTGTTAAACATGGC 1946  
DB 1902 CATTGCCACCAAGGCCGAGAGCTAGTGTGTTATTCTTTCAGCCTGGGTGTGTTTACATGCC 1961  
QY 1947 CTTCTCCAAACCTTGTTCATCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAT 2006  
DB 1962 GTTCTCTATGACCTGTTTCAACAGAGTTCCTCTGGAGTATCAAGCCCTGGAAACAACGAT 2021  
QY 2007 CACAGCTGTCTGTTTCCATATCTACGATCCAACTTACAGGATTTAAGCAACTTGAAT 2066  
DB 2022 CACAGCTGTCTGTTTCCATCTACGATCGAATCTTACGGGATTTAAGCAACTTGAAT 2081  
QY 2067 ACTTAACTTCAAGAACGGGAGTGTGATGTGAATPAGCAAAATGAAGTTTGTAAAGTCTGT 2126  
DB 2082 ACTCAGCTTCAGAAACGGGAGTGTGATCGTGAACAGCAAAAGTGGGTTTGCAGAGCGGT 2141  
QY 2127 GCGGTATAACCTCACCAGGCTGTGACGGGTCTTGGAGGATTTTGTCTGTCTGTCGAGC 2186  
DB 2142 ACCCTAACCTCACCAGGCGGTGCGCGGGTCTTGGAGATCTTGGTCTCACCGGAGC 2201  
QY 2187 CCAACAACTCCACTGGAAATAGACAGCTACTCTCTCAACATTTGAACACAGCTGATCAAGC 2246  
DB 2202 TCAAGGGCTCAATCTGGAATCGAAAGTACTCTCTCGACATTTGAACACAGCTGATCAGGC 2261  
QY 2247 AGATCCCTGCAAGTCTCTGGCTCGGCGAATTTGGCCCAATGTGTAAAGAACAGCACCGAC 2306  
DB 2262 GGAATCCCTGCAAACTCTAGACTGTGGCAATTTGGCCAGTGTGTAAAGAAATGAGTGGAC 2321  
QY 2307 TGAGGAAGCGGAGTGTCTGCTGCAAAACAGGATATGACAGCCAGGGGAGCTTGAAGCTCT 2366  
DB 2322 AGAGGAGCAGAGTGTCTGCTGACAGAGGACATGAGAGCCACGGGACCTTGGACTACCA 2381  
QY 2367 GGAACCAAGGCTCTGTGGCCCTTGGCACAAAAGGAATGCGAGGTCTCTCCAGGGAAGGAGC 2426



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Db 2382 GACCCGTGAACCTCTGTGCCCTGG---AAGACITGTGTGCGCGCGAGACAGCAAC 2438
QY 2427 TCCATGCAAGGTGCGAGATCACTCTGAAATCAAGATACAAACTAGTGTGTTAAAGATT 2486
Db 2439 TCCATGCAAGGTGCGAGATCACTCTGAAATCAAGATACAAACTAGTGTGTTAAAGATT 2498
QY 2487 CCAAAATCAACAAATCAACAGGTAAATCAGTAAAGAAATTTCTGAATTAAGTCCGCTAGA 2546
Db 2499 ACGTCAGCAA-----AATAGGTAGTCAGAAAAGAAATTTCTGAATTAAGTCCGCTAGA 2552
QY 2547 ATATGAAGAAATTAACCATCAAGATTTGGAAAGAAATTAAGAACTGAAA----- 2595
Db 2553 AITTTGAAGAAATTTGAAGACAGGAGTCTGGAGGAAATTAAGAACTGAAA----- 2612
QY 2596 -----ATGTCAATTAATCACTTAGGCTATCTCAAGAGAGATGATTTGCTT 2640
Db 2613 ATGTTGCAAACTCTGTTGAAGGAACTTTATTTCTTAAAGAAAGGTGATCTGTTCTGT 2672
QY 2641 TCTCAAGAAATGGAGACAGGCAATTTCAATGCTCATCAAAATCCAGACATACAGTCAA 2700
Db 2673 TAACCTTCTGAAAAACAGAGGAGAGATTCAGTGTCTATTGGAATACAGGCAATGTAATCAA 2732
QY 2701 CACTGGAATCAGCACACACATATTTCAATATAGAGAGTCACTGTTGCAACCCAG 2760
Db 2733 CTTTGAGACTCAG-----CATGCTTGAACAGAGCACAGGCGTGTATTGTATGA-CAG 2784
QY 2761 TAAATCTGAAAAAAGACACACTTACTTATTATTA--AAACCCCAATGCAATCAGCGAA 2818
Db 2785 TTAAGCCTGTGTTGGGGGGGGGACATATTTTGTAGTCAAACTCAAGCAATCATGGA 2844
QY 2819 ACATATTTTACTATTTCTGATGATAGTCAAAATGATCAATAGCCAGGTTGCTTCCAC 2878
Db 2845 ACACA-TTGACTATTTTGGACAGTACTC--AAGTAGCAAAAGATAAGGTAGCTTTT 2901
QY 2879 CTTCCCTGAAAAATTTACTCACAGATCATTTGCAACAGCATAGCTTACTTATTTGTTAG 2938
Db 2902 CTTTCTTTAAATTTATACATAAARCTTTTCAATTAATACAAAC-----TTGTTT 2954
QY 2939 GGAAGTCAAAATTTATGGGAACAACTTTTATATGCTAGAAAGTACATTTAAAGAT 2998
Db 2955 TGGGTTGTACAATTTAGGATCTGATTTCTTTTATATGTTAGATATACAGTTAAAGAT 3014
QY 2999 GACTACTTACGC 3010
Db 3015 TATCATTGGGC 3026

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## RESULT 14

AAA46309  
ID AAA46309 standard; cDNA; 3206 BP.

XX AC AAA46309;

XX 04-SEP-2000 (first entry)

XX cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).

XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KW chromosome q13-q15; ocular disease; retinal detachment;  
 KW chorioretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod- cone dystrophy; cone-rod dystrophy; ss.

XX Mus sp.

XX Key Location/Qualifiers  
 XX CDS 1..2130

XX /tag= a  
 XX /transl\_except= (pos: 16..18, aa: Val)  
 XX /transl\_except= (pos: 55..57, aa: Ala)  
 XX /transl\_except= (pos: 58..60, aa: Tyr)

FT /transl\_except= (pos: 73, aa: Asp)  
 FT /transl\_except= (pos: 234..236, aa: Xaa)  
 FT /transl\_except= (pos: 271..273, aa: Xaa)  
 FT /transl\_except= (pos: 403..405, aa: Xaa)  
 FT /transl\_except= (pos: 2107..2109, aa: Xaa)  
 FT /product= "interphotoreceptor matrix proteoglycan IPM150"  
 FT /note= "Xaa is an unspecified amino acid"

XX WO200026367-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025440.

XX 29-OCT-1999; 98US-00183972.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI: 2000-365616/31.

XX P-PSDB; AAY93338.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for preventing, diagnosing and treating ocular disorders such as retinal detachment and chorioretinal degeneration.

XX Claim 2; Fig 6A; 183pp; English.

XX The present sequence encodes an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome q13-q15, between markers CHLC.GATA1110 and D6S284. The IPM proteins may be used to supplement a patient's own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, chorioretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, RPE (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

XX Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;

XX Query Match 33.8%; Score 1127.2; DB 3; Length 3206;  
 XX Best Local Similarity 68.9%; Pred. No. 9.9e-291;  
 XX Matches 1824; Conservative 5; Mismatches 665; Indels 152; Gaps 15;

QY 418 TTATAGATTGAGATGTCAGGAACAGTATGGAGCATATCGGATCTTTTGGATCG 477

Db 18 TCAGGAATCAAGATATGTCAGGAATGTCGTGGGAATGATCGTATCTTTTGGNNAG 77

QY 478 CATCCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTG 537

Db 78 AATTCTCTGACACAGAGGAATATCAAGCTGGGTGAGCATCTGCCAGGAAGAACTTCTG 137

QY 538 CCTCTTTGACATTTGGAATAAATTCAGCAATTCAGGAGGACCTGATCTTCTCCAGCA 597

Db 138 CCTCTTTGACATTTGGAATAAATTCAGCAATTCAGGAGGACCTGATCTTCTCCAGCA 197

QY 598 GAGATAAACAACAGAGAAGTTTCCCTGACAGAAAGATGAAATATCTGCAGAGAGACATT 657

Db 198 GAGATAAACAACAGAGAAGTTTCCCTGAGGAAGATGAGAGCTCCATCGAGACACT 257

QY 658 GAGAGAGCTTGGTGAACCATTTGCTATTTCACAGCAATTTACATTTTCAAGACTTTGGGC 717

Db 258 GGAAGCAGCTTACTGAGAGCCCTGTGTGTACCCAC----- 290

QY 718 AGTATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAAAGTCTCACTTGGG 777  
Db 291 -----AGATGTTCCAGGATGTCCCTGGG 315  
QY 778 CTTTTCCCTCTCACTCCCTGATGACACCCCTCTCAATGAATTCGATAAATACACTCAAC 837  
Db 316 CMTTCCCACTTCCCTCTGATGACACAGACCTCAAGGAGATTCTCAGTGTCAACCTCAAG 375  
QY 838 GACACCAAGATGCCCTACACAGAAAGAGAAACAGAA-----TTGCTGTGTG 885  
Db 376 GACATTCAAAAGCCACACAGAAAGTAGAAGAACCTATTCAATGCTGTGAATTTCTCA 435  
QY 886 GAGGAGCAGAGGTGGAGCTCAGCGTCTCTCTGTGTAACAGAAAGTTCAAGCGAGCTC 945  
Db 436 TCAGAGGAGAGGTGGATTCAGCATCTCTCTGCAAAACACAGGTTCAAGCGAGAGCTC 495  
QY 946 GCTGACTCCAGTCCCACTATTTACCAGGAGCTAGCAGGAAGTCCCACTTCAGATCAA 1005  
Db 496 ACCAATCTGGGTCAACATACTACAGGAATGTGGGACAGTCCCACTCAGTTGCA 555  
QY 1006 AAGATATTAAAGAACTTCCAGGATTCMAAAATAATCCATGTGTAGGATTTAGACCAAG 1065  
Db 556 AAGATATTAAAGAACTTCCAGGATTCGAGAAATCCGTGTATTAGGATTTAGACCAAG 615  
QY 1066 AAAGAAAGAGTGGCTCAAGCTCCACAGAGATGCAATTTACGGCCATCTTTAGAGACAC 1125  
Db 616 AAAGAAAGAGTGGTCAAGCTCCACAGAAATACAGCTTTAGGCCATCTTTAAGAGGGAC 675  
QY 1126 AGTCAGAGCAAAAGCCCTGCAAGTGACCTCTCTCTTTGATTCCAACAAAATTGAA 1185  
Db 676 CATGCAGAAACAAAAGCCCTGATAGTACTCTCTCTGATTCACACAAAATTGAA 735  
QY 1186 AGTCAGAGTCTATCATGGAACCATGAGAGAGACAAAGCAACAGAAATCTATCTCA 1245  
Db 736 AGTGAAGAAATCCATCTGAGTCTATCACTACTAGATGGAGACCTGCTTTGGTAGAA 792  
QY 1246 GCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAAGCAATCTTTGGATGTG 1305  
Db 793 GCTACAGACCTCAAAAGGCTGATCAGCAAGCACTACTAGATGGAGACCTGCTTTGGTAGAA 852  
QY 1306 GGGACAAATCAGTCTCAGTGAATTTGCTGGATCACTGCCAGCCTTGGTCTGACACC 1365  
Db 853 GGGAAATTTCCATTCGGTGTGAAGTACTGGGACACT-----CTTCAGACCTGTCACT 906  
QY 1366 CAATCAGAGTGCACACATCTTTTGTCTTATACAGAGATGCTACTTTGATGTCAGAA 1425  
Db 907 GAACAGATCTGCCCAAGCCCTTGCTGTGTGTCAGAGATGCCATTTGATGTCAGAA 966  
QY 1426 CTTCTCTGTGTGAACCCAGCTTGACAGTGGAGCGAGCAGATGCTCTACCT--- 1482  
Db 967 CTTCTCTGTGTGAGCTTAGGCTTGAGCGAGTGGACAGAGATCTGAGCTGCTGGA 1026  
QY 1483 -----GACACTTCTGGTCTCCACCTGTATGCGCTCTACCTCTGCTGAGAA 1530  
Db 1027 ATGTCTCCAAAGACAGTTCTTGCTCTCCACCTGTATCAGCCTCAATTTCCCGATCAGAA 1086  
QY 1531 GCTCCACTTTCTTTATGGCATCAAGCATCTCTCTGTGATGATGATGATGATGATGAT 1590  
Db 1087 AATCTACTCTGTTA---CACCTAGATCTTCTCTAGATGCTCAAGGCCCTCC 1143  
QY 1591 ACATGSCCACTGACAGCAATGCTAGTACAGGGCTCAACATCCCAACCAAGTATTAT 1650  
Db 1144 TTGATGACCACTGGCCCAACAGCACTCATCCCAAGCCCACTCTCCCACTATCGATTAT 1203  
QY 1651 TCTGCAATCAGCAACTGGCTCTGGGAATTTACATCCCACTGCACTCTCAGATGACAGC 1710  
Db 1204 TCTACCATCGCCAAATGCTCTGGATCGTCAATGGCTGCTGCTGCTGCTGCTGCTGCT 1263  
QY 1711 CGATCAAGTGGAGGAGATAGTTCAGACACCTAGATGAATGGATCTGTCTGAC 1770  
Db 1264 GAGCTGATCAAGAGAGCCATGACAAATCCGAGACCTAGATGGCATGATGTGCTGAC 1323  
QY 1771 ACTCTGCCCACTCTGAGGTACAGAGCTCAGGAAATAGTTCTGTCTCCAGATCATTTTC 1830

Db 1324 ACCCGACCTTGTGAGAAATATCAGAACTGAGTGGATAGATTCTGCTCTGGGTGAGTTTC 1383  
QY 1831 TTGGAGATACCACTCTCTCTCAGCTTTTACAGTATATCACCACTAGTTTCTATGACCAAT 1890  
Db 1384 TTGGAGATACCACTCCATCCCAACAGTACGTTTCTATCACCACTAGTTTCTGAGACCAAT 1443  
QY 1891 GCCCCCAAGGGCGAGAGCTGTGTCTTCTCAGTCTGCGTGTGCTTAACATGGCCTTC 1950  
Db 1444 GCCCAAGGGCGAGAGCTGTGTATTCTTTCAGCCTGCGTGTGCTTAACATGGCCTTC 1503  
QY 1951 TCCAGACACTGTTCACAAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACA 2010  
Db 1504 TCTATGACCTGTCAACAGAGTCTCTGGAGTATCAAGCCCTGGAACAAAGATTTCACA 1563  
QY 2011 CAGCTGCTGTTCCATATCTAGATCCAAATCTTACAGATTTTAAAGCAATTTGAATATCTT 2070  
Db 1564 GACCTGCTGTTCCCTATCTAGATCGAATCTTACGGATTTTAAAGCAATTTGAATATCTT 1623  
QY 2071 AACTTCAGAAACGGGAGTGTGATTTGTAATAGCAAAATGAAAGTTTGTAAAGTCTGTGCG 2130  
Db 1624 AGCTTCAGAAACGGGAGTGTGATCTGAAACAGAAAGTGGGTTTGAAGGGGTATCC 1683  
QY 2131 TATAACCTCACCAGGCTGTGCAAGGCTTTGGAGATTTTCGTTCTGCTGACGCCAA 2190  
Db 1684 TACAACCTCACCAGGCTGTGCGGGTCTTGGAGATCTTCGGTCCACCGAGCTCAA 1743  
QY 2191 CAACTCCATCTGAAATAGACAGTACTCTCTCAATTTGAACAGTGTATCAAGCAAT 2250  
Db 1744 GGGCTCAATCTGAAATCGAAAGTACTCTCTCGACATTTGAACAGTGTATCAGGCGAT 1803  
QY 2251 CCCTCCAAAGTTCCTGGCTGCGGCAATTTGCCAAATGTGTAAAGAAACGAAACGAGTCAAG 2310  
Db 1804 CCCTCCAAACCTCTAGACTGTGGCAATTTGCCCAAGTGTGTAAAGATGAGTGACAGAG 1863  
QY 2311 GAAGCGAGTGTGCTGCAACAGGATATGACAGCCAGGGAGCTTGAGCGTGTGAA 2370  
Db 1864 GAAGCAGAGTGTGCTGACAGAGGATGAGAGCCACCGGACCTTGAGTACAGAGC 1923  
QY 2371 CCAGGCTCTCTGGCCCTGGCAACAAAGAAATGCGAGGTCCTCCAGGGAAGAGGAGCTCCA 2430  
Db 1924 CTGAACCTCTGTCCCTCTG---AAAGACTTGTGTGGCCGCGCGAGAACAGCACTCCA 1980  
QY 2431 TGCAGTTGCCAGATCACTCTGAAATCAAGCATACAAACTAGTTTAAAGATTTCCAA 2490  
Db 1981 TGCAGGCCACAGATCACTCTACAAACCAAGCTCAGGAACCTGTTGTAAAGATAGCT 2040  
QY 2491 AATCAACAAATTAACAGGTAATCAGTAAAGAAATTTCTGAATTTACTGACCGTGAATAT 2550  
Db 2041 CAGCA-----AATAGGTAGTCAAGAAAGAAATTTCTAACTATCAGCTATAGGATTT 2094  
QY 2551 GAAGATTTAAACCATCAAGATTTGGAAAGGAAATTTAAAGAACTGAAATTTGA-CAAATATCA 2609  
Db 2095 GAAGAAATTTGAARACAGGAGTGGGAGGAAATTTAAAGCTGGAATCATATGCAATTTATGT 2154  
QY 2610 CTTAGGCTATCTCAAGAGAGATGATTTGCCCTTTCTAAGGA----- 2649  
Db 2155 TGCAACTCTGTTGAAGGAAACCTTTATTTCTTAAAGAAAGGTGTATCTGTCTGTGTTAAC 2214  
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Db 2331 GGTGGGGCGGGGGCACATATTTTAGTCAAACTC---AAAGCAATCATTTGGAACACA- 2387  
QY 2825 TTTTACTATTTCTTGGATGATGATCAAAATGATCATAGCCAGGTTTGTCTTCCACTTCC 2884

Db 2398 TTGACTATTTTGGACAGTACTC--AAGTAGCAAGATAAGGTAGCTTTTCTTTCT 2445  
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## RESULT 15

ID ADA14849 standard; cDNA; 1726 BP.

AC ADA14849;

DT 06-NOV-2003 (first entry)

XX Mouse interphotoreceptor matrix component, IPMC, 150 isoform D cDNA.

DE ss: Gene; mouse: IPMC 150 isoform D; gene therapy;  
 XX interphotoreceptor matrix component; IPMC; ocular disorder;  
 XX macular degeneration; photoreceptor death; retinal detachment.

OS Mus sp.

FH Key Location/Qualifiers

FT CDS 140..1540

FT /\*tag= b

FT /product= "IPMC 150 isoform D"

FT /\*tag= a

FT /label= Signal\_sequence

FT 200..1537

FT /\*tag= C

FT /label= Mature\_IPMC\_150\_isoform\_D

XX US2002160954-A1.

XX 31-OCT-2002.

XX 08-NOV-2001; 2001US-00007270.

XX 29-OCT-1998; 98US-00183972.

XX 29-OCT-1999; 99US-00430195.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2003-238235/23.

XX P-PSDB; ADA14850.

XX New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.

XX Claim 3; Page 43-44; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene

CC expression in a cell. The present sequence represents cDNA encoding mouse  
 CC interphotoreceptor matrix component, IPMC, 150 isoform D.

XX Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;

SQ Query Match 16.0%; Score 534; DB 7; Length 1726;

Best Local Similarity 72.0%; Pred. No. 5.5e-132;

Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;

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Db 171 TTTTGGGATTTTCTCCAAGTTCAAGGAATCAAAAGTATGTCAAGAGTCGTGTGGGAAG 230

QY 456 CATATCGGATCTTCTCGATCGATCCCTGCACAGAGGGAATATCAGACACTGGGTCAGCA 515

Db 231 CATATCGTATCTTCTCGACCGAATCTCTGACAGAGGAATATCAAGCTGGGTCAGCC 290

QY 516 TCTGCCAGAGAGACTTCTTCTGCTCTTTTGACATTTGGAAAAAATCTTACGAATTTCCCAAG 575

Db 291 TCTGCCAGAAAAAACCTTCTGCTCTTTTGACATTTGGAAAAAATCTTACGAATTTCCCAAG 350

QY 576 AGCACTCGATCTTCTCCAGCAGAGAGATAAACAAGAGAGTTTCCCTGACAGAAAAAGATG 635

Db 351 AGCACTAGATCTTCTTTCAGCAGAGATAAACAAGAGAGTTTCCCTGAGGAGAAAGATG 410

QY 636 AAATATCTGCAGAGAGACATTTGGAGAGCGCTGTGAAACCAATTTGTCATTTCAACAGCAA 695

Db 411 AGACAGCTCCATGGAGACACTGGAAGCACCTACTGAAGCCCTGTGTATCCAC----- 465

QY 696 TCTACATTTCAAAGACTTGGCAGTATTCTAAGAAAAACCTTCAGAAAGCAAAATTCAGA 755

Db 466 -----AGAA-----AGA 468

QY 756 TGTGCCAAACGTCTCACTTGGGCTTTCCCTCTCACTCTCTGATGACACCTCTCTCAATGA 815

Db 469 TGTTCAGAGATGTCCTGTGGGCCATTTCCCACTTCTCTGATGACACAGACCTCAAGGA 528

QY 816 AATTCTCATTAATACATCTCAACAGACACCAAGATCCCTTACAAAGAGAGAGAAACAGAA-- 873

Db 529 GATTCAGTGTCACTCCCTCAAGGACATTCAAAAGCCCAACAGAGAAAGTATAACAGAAACC 588

QY 874 -----TTCCCTGTGTGGAGGAGCAGAGGTGGAGCTCAGCGTCTCTCTGTGTA 923

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QY 924 CCAGAAGTTCAAGGCAGAGCTCGCTGACTCCCACTCCCAATATTACCAGAGCTAGCAGG 983

Db 649 CCACAGGTTCAAGGCAGAGCTCACCACTCTGGGTCACTACTTACCAGAGACTGTGTGG 708

QY 984 AAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAGGATTCAAAAAATCCA 1043

Db 709 ACAGTCCCACTGCAGTTGCCAAAGATATTAAAGAACTTCCAGGATTCGAGAAATCCG 768

QY 1044 TGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACT 1103

Db 769 TGTATTAGGATTTAGACCAAGAAAGAAAGATGGTTCAAGTCTCCAGAAATACAGCT 828

QY 1104 TAGCGCATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTACCTCTCTGTC 1163

Db 829 TATGCCATCTTTAAGAGGAGACCATGCAAGCAAAAGCCCTGATAGTCTATCTACTGTC 888

QY 1164 TTTTGTATCCCAAAATTCAGAGTGGAGAGTCTATCATGGAACTCATGGAGAGAGCA 1223

Db 889 TCTTGTATCCCAAAATTCAGAGTGGAGAGTCTATCATGGAGTCTATTCATGGAGAGCA 945

QY 1224 GCAACCAAAATCTATCTCAGCTACAGACTCAAGACCTCAAAAGCTCATCAGCAAAAGCACTAGA 1283

Db 946 ACAACCAAAAGCTTACTCAGCTACAGCTCAAGACCTCAAAAGCTCATCAGCAAAAGCACTAGA 1005

QY 1284 GGAAGAACATCTTTGGATGTTGGGACAAATTCAGTTCATGTATGAAATTCGTGGATCACT 1343

Db 1006 TGGAGACCTGTCTCTGGTAGAAGGGAAAAATTCATTCGGTGTGATGAAGTACTTGGGACACT 1065



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 20:29:14 ; Search time 4968 Seconds  
(without alignments)  
4790.692 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLSTRATFVFIFLQVQ.....NSELLTVEEFPHQWEGN 797

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
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Database :

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3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1683	40.9	1647	29	AY415973 Mus muscu
3	1054	25.6	626	13	BQ63265 HG33004.Y
4	971	23.6	1587	29	AY415972 Pan trogl
5	955	23.2	598	13	BQ636596 hdl1h02.Y
6	902	21.9	3713	29	AY418611 Homo sapi
7	893	21.7	690	13	BX510244 DKFZ0686P
8	829	20.1	963	13	BU506195 AGENCOURT
9	819.5	19.9	3734	29	AY418613 Mus muscu
10	817.5	19.9	3713	29	AY418612 Pan trogl
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12	799	19.4	472	13	EX097138 BX097138
13	759	18.4	510	9	AL713229 DKFZ0686P
14	751	18.2	618	14	CA391789
15	738	17.9	561	14	W26960
16	730.5	17.7	914	13	BX743511
17	714.5	17.4	824	12	BI738723
18	708	17.2	797	11	AK020862
19	686	16.7	422	12	BM726533
20	685	16.6	886	14	CF549501 AGENCOURT
21	674	16.4	753	12	BI735383
22	649	15.8	448	12	BM681190
23	637	15.5	393	13	BQ636351
24	636	15.4	851	12	BI732865
25	634	15.4	836	12	BI752112
26	631	15.3	843	13	BX743512
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28	612	14.9	405	14	H38604
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44	273	6.6	3250	11	BC026456
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# ALIGNMENTS

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DEFINITION Homo sapiens IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
1665 bp DNA linear GSS 17-DEC-2003  
ACCESSION AY415971  
VERSION AY415971.1 GI:39771931  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1665)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1665)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1. (bases 1 to 626)  
 Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 Expressed sequence tag analysis of human retina for the NEIBank  
 Project: Rebindin, an abundant, novel retinal cDNA and alternative  
 splicing of other retina-preferred gene transcripts  
 Mol. Vis. 8 (4), 196-204 (2002)  
 22103461  
 MEDLINE  
 12107411  
 COMMENT  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
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 the protocols of the SuperScript Plasmid System full  
 details of which are contained in the manufacturer's  
 instruction manual (<http://www.lifetech.com/>). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor

[5'-PGACTAGTTCTAGATCCGAGCGCGCCGCT(T)15-3']. EST analysis  
 was performed on the unamplified library at the NIH  
 Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:  
 Pred. No.: 2,378-94 Length: 626  
 Score: 1054.00 Matches: 208  
 Percent Similarity: 100.00% Conservations: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 25.60% Indels: 0  
 DB: 13 Gaps: 0

US-10-007-270-2 (1-797) x BQ639265 (1-626)

QY 260 GlnGluLeuAlaGlyLysSerGlnLeuMetGlnIlePheLysLeuProGly 279  
 Db 3 CAGGAGCTAGCAGGAGGAGTCCCAACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGA 62  
 QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
 Db 63 TTCAAAAAATCCATGTGTAGGATTTAGACCAAAAGAAAGATGGCTCAAGCTCC 122  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 Db 123 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAGCAAAAGCCCTGCA 182  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339  
 Db 183 AGTGACCTCTCTGTTTGTATCCCAAAATTTGAAAGTGGAGAGTCTATCATGGAAACC 242  
 QY 340 MetGluGluAspLysGlnProGluIleTyrIleThrAlaThrAspLeuLysArgLeuIle 359  
 Db 243 ATGGAGGAGGACAAAGCAACAGAAATCTATCTCAGCTACAGACCTCAAAAGCTGATC 302  
 QY 360 SerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
 Db 303 AGCAAGCAGCTAGAGGAGAACAAATCTTTGGATGTGGGACAAATTCAGTTCACGTGATGAA 362  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 Db 363 ATTGCTGATCAGCTGCCAGCTTTGGTCTTGACACCAATCAGAGCTGCCACATCTTT 422  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
 Db 423 GCTGTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTGTGTGAACCCAGCTT 482  
 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMet 439  
 Db 483 GAGACAGTGGACGAGGAGGAGCATGGTCTACCTGACACTTCTTGGTCTCCACTGCTATG 542  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
 Db 543 GCCTCTACCTCCCTGTGAGAAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTCTG 602  
 QY 460 ThrAspGlnGlyThrThrAspThr 467  
 Db 603 ACTGATCAGGACCCACAGATACA 626

RESULT 4

AY415972

LOCUS

DEFINITION

AY415972

ACCESION

AY415972

VERSION

AY415972.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AY415972 1587 bp DNA linear GSS 17-DEC-2003  
 Pan troglodytes IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.

AY415972 GI:39771932  
 Pan troglodytes (chimpanzee)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 1587)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,



Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

JOURNAL  
 Science 302 (5652), 1960-1963 (2003)  
 PUBLISHED  
 14671302  
 REFERENCE  
 2 (bases 1 to 1587)

AUTHORS  
 Clark, A.G., Ghanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.

TITLE  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

COMMENT  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment

## FEATURES

source

Location/Qualifiers

1..1587

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

<1..>1587

/gene="INFG1"

/locus\_tag="HCM5735"

## ORIGIN

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 Percent Similarity: 45.27% Conservative: 0  
 Best Local Similarity: 45.27% Mismatches: 289  
 Query Match: 23.59% Indels: 0  
 DB: 29 Gaps: 0

US-10-007-270-2 (1-797) x AY415972 (1-1587)

QY 270 MetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArg 289  
 Db 1 ATGCAAAAGATATTTAAGAACTCCAGGATTCAGAAATCCATGCTAGGATTTAGN 60  
 QY 290 ProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIlePheLys 309  
 Db 61 NNN 120  
 QY 310 ArgHisSerAlaGluAlaLysSerProLaserAspLeuLeuSerPheAspSerAnlys 329  
 Db 121 NNN 180  
 QY 330 IleGluSerGluGluValTyHisGlyThrMetGluGluAspLysGlnProGluIleTyR 349  
 Db 181 NNN 240  
 QY 350 LeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeu 369  
 Db 241 NNN 300  
 QY 370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
 Db 301 NNN 360  
 QY 390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
 Db 361 GACACCAATCAGAGCTGCCACATCTTTGCTGTATACAGAGNATGCTACTTTGAGT 420  
 QY 410 ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeu 429  
 Db 421 CCAGAACTTCCTTTGTTGTAACCCAGCTTCAGACAGTGGACGAGCAGACATGGTCTA 480  
 QY 430 ProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
 Db 481 CCTGNN 540

RESULT 5

QY 450 PhePheMetAlaSerSerIlePheSerIleThrAspGlnGlyThrThrAspThrMetAla 469  
 Db 541 NNN 600  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTySerAlaIle 489  
 Db 601 NNN 660  
 QY 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSer 509  
 Db 661 NNN 720  
 QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
 Db 721 NNN 780  
 QY 530 ProSerGluValProGluLeuSerGluTyTrValSerValProAspHisPheLeuGluAsp 549  
 Db 781 CCATCTGAGGTACCAGAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTGGAGGAT 840  
 QY 550 ThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAlaProLys 569  
 Db 841 ACCACTCTGTCTGTCTTTACAGTATATCACCAGTATGTTCTATGACCATTTGCCCAAG 900  
 QY 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589  
 Db 901 GGCCGAGAGCTGGTAGTGTCTTCAGTCTCGTGTGCTAACATGGCCCTTCTCAACGAC 960  
 QY 590 LeuPheAsnLysSerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
 Db 961 CTGTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGAGCAANNNNNNNNNNNNNNCTG 1020  
 QY 610 ValProTyLeuArgSerLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
 Db 1021 GTTCCATCTACGATCCCAATCTNNCAGGATTTAAGCAACTTGAATACTTAACCTCAGA 1080  
 QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyAsnLeu 649  
 Db 1081 AACGGAGTGTGATTTGTAATACCAAAATGAAGTTTCTAAGTCAGTCGGTATNNNNNC 1140  
 QY 650 ThrIleAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
 Db 1141 ACCAAGCTGTGCACGGGTCTTTGGAGGATTTTCGTCTGCMNCAGCCCAACCACTCCAT 1200  
 QY 670 LeuGluIleAspSerTyTrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 699  
 Db 1201 CTGGAATAGANACNACTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260  
 QY 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
 Db 1261 NNN 1320  
 QY 710 CysArgCysLysProGlyTyTrAspSerGlnGlySerLeuAspGlyLeuProGlyLeu 729  
 Db 1321 NNN 1380  
 QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
 Db 1381 NNN 1440  
 QY 750 ProAspHisSerGluAsnGlnAlaTyTrLysThrSerValLysPheGlnAsnGlnGln 769  
 Db 1441 NNN 1500  
 QY 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyTrGluGluPhe 789  
 Db 1501 NNNNNNNNNNGTAACTCAGTAAAGAAATCTGAATTACTGACCGTAGAATATGAAGATTT 1560  
 QY 790 AsnHisGlnAspTrpGluClyAsn 797  
 Db 1561 AACCATCAAGATTGGGAAGGAAAT 1584

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BQ636596
LOCUS      598 bp      mRNA      linear      EST 15-JUL-2002
DEFINITION hdl1h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
Homo sapiens cDNA clone hdl1h02 5', mRNA sequence.
ACCESSION BQ636596
VERSION   BQ636596.1 GI:21761055
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 598)
Wistow,G., Bernstein,S.I., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D., and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank
project: Retbinding, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
22103461
MEDLINE
PUBMED
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 11 row: h column: 02
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hdl1h02"
/tissue_type="Retina"
/dev_stage="adult"
/lab_host="EMDH108"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/notes="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioerve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGCTAGTCTAGTCGAGCGCGCC(7)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."]
ORIGIN
Alignment Scores:
Pred. No.: 1..66e-84 Length: 598
Score: 955.00 Matches: 190
Percent Similarity: 98.47% Conservatives: 3
Best Local Similarity: 96.94% Mismatches: 3
Query Match: 23.20% Indels: 0
DB: 13 Gaps: 0
US-10-007-270-2 (1-797) x BQ636596 (1-598)
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Db 11 TCGCCTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTGACAGCTCCACCTTCTTT 70
QY 452 MetAlaSerSerLeuPheSerLeuThrAspGlyThrThrThrAspThrMetAlaThrAsp 471
Db 71 ATGGCATCAGCATCTTCTCTGACTGATGACAGGACACACAGATATATGGCCACTGAC 130

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QY 472 GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491
Db 131 CAGACAATCTAGTACAGGCGGCACCATCCCCACAGTGATTATTTCGAATCAGCCAA 190
QY 492 LeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGly 511
Db 191 CTGGCTCTGGGAATTTTCATCCCTCCATCTTCAGATGACAGCGCATCAAGTCAGT 250
QY 512 GlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSer 531
Db 251 GCGCAAGATATGCTCAGAGACCTAGATGAATGGATCTGTCTGACACTCTCTGCCCATCT 310
QY 532 GluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThr 551
Db 311 GAGGTACACAGACTCAGCGAATATGTTCTGTGCCAGATCATTTCTTGGAGATACCACT 370
QY 552 ProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProlysglyArg 571
Db 371 CCTGTCTCAGCTTACAGTATATACCACTAGTCTATGACCATGCCCCACAGGCGCA 430
QY 572 GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591
Db 431 GAGCTGGTAGTGTCTTCAATCTCGTGTCTTCAATCTCGTGTCTTCAATCTCGTGTCT 490
QY 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuValPro 611
Db 491 AACAAAGACTCTCTGGAGTACCGAGCTCTGGAGCAACATTCACACAGCTCTGGGTCCA 550
QY 612 TyrLeuArgSerAsnLeuThrGlyPheLeuGlnLeuGluLeuLeuLeuLeu 627
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DEFINITION Homo sapiens IMPC2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY418611
VERSION   AY418611.1 GI:39774571
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3713)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 3713)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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ORIGIN

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 Query Match: 21.91% Indels: 405  
 DB: 29 Gaps: 34

US-10-007-270-2 (1-797) x AY418611 (1-3713)

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 DB 11 TTCTCTTTTGGGAAGATTCTCTGGTATTTCGTTG-ATATTGTCTGTATAGACGAC 69  
 QY 22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39  
 DB 70 TTTCATCATTAACACCAACACCTACTTATCT-ATAGAGGAGATCCAGAACCCCAAG 126  
 QY 40 -----ProArgAsnGluThr-----ThrGluSer 47  
 DB 127 AGTGCAGTTTCTTTCTCTGCTGGAAGATCAACAGACCTTTCTCTAGCTACCAAAAG 186  
 QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67  
 DB 187 AAACAGCCTCTGGACCCGACAGAAACTGAAAGACAGTGGTTA-----ATCAGA 234  
 QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87  
 DB 235 AGCGGAGATCTATTCTGTTCTTAATGGAGTGAATACTGCCAGATGAAGTGTGCA 294  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107  
 DB 295 GAGGTGTGGCAAAATCATGTGAAGTATTTAAAGTCCGAGTGTGTCAAGAAAGTGTCTGG 354  
 QY 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127  
 DB 355 GAAGCCTTCAGCACTTTTGGATCGACTTCTGGCGTGAAGATATCATTAATCTGGATG 414  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
 DB 415 AATTTGTGTGGATGGAGTCAACAGTATATTTGAATGGGCACAAATTTTAGTGAATCT 474  
 QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 DB 475 GTGGAACTAGAACGTTAATCATGAAGAACTGACTTAT-----GCCAAG 519  
 QY 168 AspGluIleSerAlaGluLysThrLeuGlyGluPro-----GlyGluThrIleVal 184  
 DB 520 GAAACTGTAAAGCAGCTCTGAA--CTGTCTCTCCAGTTCCTGTGTGTGTACTTCAACA 576  
 QY 185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 DB 577 TTGGGAGACACTACTCTCAGTGT-----CCATCCAGAGAGTGGACGCGCTATGAA 627  
 QY 201 -----ProAspAspThrLeuLeuAsnGluIleLeuAsp 211  
 DB 628 GGTGCTCAGAGACGAGCTTGGAAAGCCAGAGAGATATAGCAATGAAT---GAG 684  
 QY 212 AsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeu 231  
 DB 685 AATGTGTATAGAAGAACCCACAAACACGAGGTGAACAGATTCGAGAATTC----- 735  
 QY 232 GluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeu 251  
 DB 736 -----AGTATCCACTTTTGGGAGAGCAGTACAGGGAAGAACTA 774  
 QY 252 AlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGln 271  
 DB 775 CAGGATTCCTCCAGCTTCCACCACGACCTTGAAGAGAAATTTATTTTCAGAGGTGAA 834  
 QY 272 LysIlePheLysLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLys 291

DB 835 AATGCATTACTGGGTACACGAGCTACAAGAAATCGTGACTGTAATTTAGNNNNNN 894  
 QY 292 LysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311  
 DB 895 NNNNNNNNNNTGGCTAGATGTTTACTATGCACTTACC-----TTC 939  
 QY 312 SerAlaGluAlaLysSerProAlaSer---AspLeuLeuSerPheAspSerAsnLysIle 330  
 DB 940 AATGCTGAGGCCATCAGCAATACCACTGGGACCTATTAGCCTTCTCAACACAGGTG 999  
 QY 331 GluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeu 350  
 DB 1000 GAAAC-----CATGGCTGTGAACTGATGATATAACCACTGTGTATTAT 1047  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlu----- 365  
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 QY 365 ----- 365  
 DB 1108 AACTTCTCTGTAATCCAGATCCTGATTCTCCTGAGCTTATCAATGTGAGAGAGTTTG 1167  
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 QY 378 -----AspGluIleAla 381  
 DB 1228 TCATCTATTCTGGATAATACCTTTCAAGGTGCATGCCCTCAGCAGATGAATCATCAC 1287  
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 QY 392 GlnSerGluLeuPro----- 396  
 DB 1348 TGCTCAGAAAGCTCTTGGGTGATTAGTGTCTACACAAATTAGCCTTTCCCTCGAAG 1407  
 QY 396 ----- 396  
 DB 1408 ATGGGCTCAGCTCTCCCCAGAGGTTTAGAGGTAGCAGCTTGACTCTTCACTTGTCT 1467  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 DB 1468 ACCCGGCGAGTGTCTCAGACTGGCTTGCCTGTGGCTTCTGAGGAAAGGACTTCTGTGATCT 1527  
 QY 411 GluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu----- 426  
 DB 1528 CACTTG-----GTAGAAGATGGATTAGCCAATGTTGAAGAGTCAAGAGATTTCTTTCT 1581  
 QY 427 ---HisGlyLeuProAspThrSerTrpSerProAlaMetAlaSerThr----- 442  
 DB 1582 ATTGATTCACTGCTTCAAGTTTCACTCAACCTGTGCCAAAGAAACAATACCATCC 1641  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 DB 1642 ATGGAAGACTGTGATGTGCTTAACTTTACCATATCTGACCTCTTCTATACATTTT 1701  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
 DB 1702 GCTTGGACTCTTGACCTCCAAAGTCAAGACCAATTAAGAGTGAGCCCTTCTCTGCCA 1761  
 QY 471 AspGlnThrMet----- 474  
 DB 1762 GATGCATCCATGGAAAAAGAGTTAATATTTCACGCTGGTTTAGGTTCAAGGCTCTGGCAA 1821  
 QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 DB 1822 AAGTAGATCTGATTACTTGGCCATGGAGTGAGACTTCATCA---GAGAAGAGCGCTGAA 1878  
 QY 495 GlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGlyGlyLeuAsp 514  
 DB 1879 CCACGTGCCAAGCGGTGGCTTGAAGATGATGATTCACTTTTGGCCAGCTGAGATTGAAGAC 1938

QY 515 -----MetValArgHisLeuAspGluMetAsp----- 523  
 Db 1939 AAGAACTAGTTTGTAGTTGCACAAATCGATTCACAGACCACAAATTAGTAGCACTCAAAA 1998  
 QY 523 ----- 523  
 Db 1999 TATGAACATGATGACAGATCCATACACTTTCCAGAGGAAGAGCCTCTTAGTGGCCCTGCT 2058  
 QY 524 -----LeuSerAspThrProAlaPro----- 530  
 Db 2059 GTGCCATCTTCGAGATATCGAGCTGAATCTCGCTCTTAACCCCTCCCAAGCACATA 2118  
 QY 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550  
 Db 2119 TCAGAAGTACCTGTGTGTGATGATTACTCAGTTACCAAGCACCTCTTTACTACTGACATCT 2178  
 QY 551 ThrProValSerAla----- 555  
 Db 2179 GTACCAATCTCTGCTCTTACTGTATAATCATGACGACAGATGCCATCTTAAGGGAGGAT 2238  
 QY 556 LeuGlnTyrIleThrThrSerSer----- 563  
 Db 2239 ATGGAACAAATTACTGAGTCATCCAACTAATGAATGTTTACAGAGTGAAGTTCAATGGTA 2298  
 QY 564 -----MetThrIleAlaProLysGlyArgGlu----- 572  
 Db 2299 AAGCCAGATATGCAAACTTTGTGACTATATTCGCAATTCAGAGAGTTTGGACAAGA 2358  
 QY 572 ----- 572  
 Db 2359 ACTTCTCCCTAGAGAAATTGTCAGAGACATATTGGCAAGTACACACAGAGTGTGAC 2418  
 QY 572 ----- 572  
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 QY 572 ----- 572  
 Db 2479 CTAGAGATGAAGTAATTATGGGTGTACAGGATATTTGGTAGAAGTGAACCGGATAGGC 2538  
 QY 572 ----- 572  
 Db 2539 ACAGATTACTATCATGCTGAGCAAGTCCAAAGTCCAAAGCAAAATGGCAAGTTGGTAGTTATGTG 2598  
 QY 572 ----- 572  
 Db 2599 GAAATGTCAACAAGTGTCTACTCCACAGAGATGGTTAGTGTGGCTTGGCCCAAGAGGA 2658  
 QY 573 -----LeuValValPhePheSerLeuArg 580  
 Db 2659 GGAGATGACTTGAGTTATACCCAGACTTCAGGAGCTTTGGTGGTTTCTTCAGCCTCCGA 2718  
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 Db 2779 CTGGAGCAAGATCTTAGAATTTGGTTTCCCTATCTCCAGTCAAAATCTCAGCGGGTTC 2838  
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 QY 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719  
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 DEFINITION DKFZp686p2496\_5', mRNA sequence.  
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 VERSION BX510244.1 GI:32050551  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 690)  
 AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
 Wewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and  
 Wiemann, S.  
 TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,  
 Wellenreuther, R., et al.)  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: MIPS  
 MIPS  
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by DKFZ (German Cancer Research Center,  
 Heidelberg/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No si sequence available.  
 This clone (DKFZp686p2496) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
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 Score: 893.00 Matches: 168  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 21.69% Indels: 0  
 DB: 13 Gaps: 0  
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Db 187 ATGTAATTGGAAACTAGACAGCTATTTTGGTTTGGATTTTCTCCAAAGTTCAGGA 246

Qy 21 ThrlyAspSerleAsnileTyHisSerGluThrlyAspSerleAspAsnProPro 40

Db 247 ACCAAAGATATCTCCATTAACATATACCATTCCTGAAACTAAAGACATAGACATCCCCCA 306

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Db 367 TTCGATTGGCAAGCATCGAACAAAAGATCGCATTTTCCACCGGGGTTAAAGTC 426

Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyTrArgLeuArg 100

Db 427 TGTCCACAGGAATCCATGAACACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 486

Qy 101 ValCysGlnGluAlaValTrpGluAlaTyTrArgGilePheLeuAspArgileProAspThr 120

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Db 547 GGGGATATACAGACTGGGTGACATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATT 606

Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgileLysGln 160

Db 607 GGAAPAAACTTCAGCAATTCAGAGAGACCTGGATCTTCTCCAGCAGAGAATAAAACAG 666

Qy 161 ArgSerPheProAspArgLysAsp 168

Db 667 AGAAGTTTCCCTGACAGAAAAGAT 690

RESULT 8

LOCUS BU506195

DEFINITION AGENCOURT\_10015502 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6494245

ACCESSION BU506195

VERSION BU506195.1 GI:22812428

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 963)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone Distribution by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L14M14050 row: c column: 14  
High quality sequence stop: 637.

FEATURES

source

1..963

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/tissue\_type="retina"

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full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

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Pred. No.: 1.33e-71 Length: 963  
Score: 829.00 Matches: 182  
Percent Similarity: 74.13% Conservative: 30  
Best Local Similarity: 63.64% Mismatches: 65  
Query Match: 20.14% Indels: 11  
DB: 13 Gaps: 2

US-10-007-270-2 (1-797) x BU506195 (1-963)

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Db 178 ATCAAGATACCTCTATTAATATTTCAGTTCTGAAATTAATAAATAGACAAACCCCA 237

Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyLysMetSerThrMetArgArgile 60

Db 238 AGAATCAACAATTAAGAAAGTACTTCAACAGTGCACAAAGTGTCAACCATGAAACGAATA 297

Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyVallyVal 80

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Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyTrArgLeuArg 100

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Qy 121 GlyGluTyGlnAspTrpValSerleCysGlnGlnGluThrPheCysLeuPheAspille 140

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RESULT 9	AY418613	3734 bp	DNA	linear	GSS 17-DEC-2003
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DEFINITION	Mus musculus IMPG2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY418613				
VERSION	AY418613.1	GI:39774573			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 3734) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
TITLE	Science 302 (5652), 1960-1963 (2003)				
JOURNAL	14671302				
PUBMED	2 (bases 1 to 3734)				
REFERENCE	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission				
AUTHORS	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
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DB:	29	Gaps:	33		
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QY	98	ArgLeuArgValCysGlnGluAlaValTpdGluAlaTyrArgilePheLeuAspArgile	117		
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## RESULT 10

AY418612

LOCUS

DEFINITION

Pan troglodytes

genomic survey sequence.

ACCESSION

AY418612

VERSION

AY418612.1

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes

REFERENCE

1 (bases 1 to 3713)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, P., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

AY418612 3713 bp DNA linear GSS 17-DEC-2003  
 Pan troglodytes IMPG2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.

AY418612.1 GI:39774572  
 GSS.  
 Pan troglodytes (chimpanzee)  
 Pan troglodytes  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 1 (bases 1 to 3713)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, P., Murphy, B.,  
 Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,





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QY 516 ValArgHisLeuAspGluMetAsp-----523
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Db 2794 TTGAATTTGCTGTTTCCCTATCTCCAGTCAAACTCTCAGGGGTTCCAGAACTTAGAATC 2853
QY 626 LeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerVal 645
Db 2854 CTCAACTTCAGAAATGGCAGCATTTGTGTGTGAACAGCCGATGAAGTTTGGCAATCTCTGC 2913
```

```
QY 646 ProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaAla 665
Db 2914 CTTCTCAACGTCACAAATCGGTGTACATGATTCTGGAAGACTTTTGTACCACCTGCCTAC 2973
QY 666 GlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAla 685
Db 2974 AATACCATGAACTTGGCTATTGATAAATCTCTTGTATGGGAATCAGGTGATGAAGCC 3033
QY 686 AspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThr 705
Db 3034 AACCTTTCAGAGTTTCAGGCCTGTAATGAATTTTCAGAGTGTCTGGTCAACCCCTGGAGT 3093
QY 706 GluGluAlaGluCysArgCysLysProGlyTyrAspSerGln-----Gly 720
Db 3094 GGAGAAGCAAGTGCAGATGCTTCCCTGGTTACTGAGTGTGGAAGAACGCCCTGTGAG 3153
QY 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740
Db 3154 AGTCTGTGTGACCTACAGCCCTGACTTCTGCTTGAATGATGGAAG---TGTGACATTATG 3210
QY 741 GlnGlyLysGlyAlaProCysArg 748
Db 3211 CCTGGGCACGGGCCATTTGTAGG 3234
RESULT 11
CA393958 508 bp mRNA linear EST 06-NOV-2002
CA393958
LOCUS c84904.y1 Human Retinal pigment epithelium/choroid cDNA
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs44904
5', mRNA sequence.
ACCESSION CA393958
VERSION CA393958
KEYWORDS EST.
SOURCE CA393958.1 GI:24728064
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human RPE/choroid for the
NEIBank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
JOURNAL Mol. Vis. 8 (4), 205-220 (2002)
MEDLINE 22103460
PUBMED 12107410
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 44 row: g column: 04
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs44904"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMD108"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"
/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
```

Plasmid System (Invitrogen Corp.  
 <http://www.invitrogen.com/>). The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (MISC)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.18e-70 Length: 508  
 Score: 815.00 Matches: 163  
 Percent Similarity: 97.02% Conservative: 0  
 Best Local Similarity: 97.02% Mismatches: 5  
 Query Match: 19.80% Indels: 0  
 DB: 14 Gaps: 0

US-10-007-270-2 (1-797) x CA393958 (1-508)

Qy 418 GlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProPro 437  
 Db 3 CAGCTTGAGACAGTGGACGAGCAGAGCATGGTCTACCTGACATCTTTGGTCTCCACT 62  
 Qy 438 AlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePhe 457  
 Db 63 GCTATGGCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTC 122  
 Qy 458 SerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValPro 477  
 Db 123 TCTCTGACTGATCAAGCACCACAGATACATGAGGCACATGACACACATGCTAGTACA 182  
 Qy 478 GlyLeuThrIleProThrSerAspTrpSerAlaIleSerGlnLeuAlaGlyIleSer 497  
 Db 183 GGGCTCACCATCCCAACCACTGATTTCTTGAATCAGCAACTGGCTCTGGGAATTTCA 242  
 Qy 498 HisProProAlaSerSerAspSerArgSerSerAlaGlyGlyGluAspMetValArg 517  
 Db 243 CATCCACCTGATCTTCAGATACAGCCGATCAAGTCAGGTCGAGATGCTGATGTCAGA 302  
 Qy 518 HisLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSer 537  
 Db 303 CACCTAGATGAATGGATCTGTGACACTCTCTGCCCATCTGAGTACCAGAGCTCATC 362  
 Qy 538 GluTyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557  
 Db 363 GAATATGTTCTGTCCACATCATTTCTTGGAGGATACACCTCTGTCTCAGCTTTACAG 422  
 Qy 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyValGluLeuValValPhePhe 577  
 Db 423 TATATCACCATAGTCTTATGACCATTTGCCACAGGGCCGATAGCTGGTAAAGTTCTTC 482  
 Qy 578 SerLeuArgValAlaAsnMetAla 585  
 Db 483 AGTCTCGTGATGCTAACATGGCC 506

RESULT 12  
 BX097138  
 LOCUS  
 DEFINITION  
 EX097138 Soares retina N2b4HR Homo sapiens cDNA clone  
 EX097138 IMAGE:190666, mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 AUTHORS  
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radelof, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 TITLE  
 JOURNAL  
 Unpublished (2003)  
 COMMENT  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGp998N11359.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTTCACACAGGAACAGCTATGAC.

## FEATURES

## source

1. 472  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGp998N11359 ; IMAGE:190666"  
 /sex="male"  
 /tissue\_type="retina"  
 /dev\_stage="55 year old"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares retina N2b4HR"  
 /notes="Organ: eye; Vector: p77T3D (Pharmacia) with a  
 modified polylinker; site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TGTTCACATCTGAAGTGGAGCGCGCTTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified p77T3 vector  
 (Pharmacia). The retinas were obtained from a 55 year old  
 Caucasian and total cellular poly(A)+ RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the  
 University of Toronto. Library constructed by Bento  
 Soares and M.Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.13e-69 Length: 472  
 Score: 799.00 Matches: 156  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 19.41% Indels: 0  
 DB: 13 Gaps: 0

US-10-007-270-2 (1-797) x BX097138 (1-472)

Qy 373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392  
 Db 3 ACAATTCACTTCACTGATGAATTTGCTGGATCACTGCCAGCCTTTGGTCTGCACACCAA 62  
 Qy 393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412  
 Db 63 TCAGAGTCCCACTCTTTTGTCTGTTTAAACAGAGGATGCTTGTAGTCCAGAACTT 122  
 Qy 413 ProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr 432  
 Db 123 CCTCTGTTGAACCCCACTTTCAGACAGTGGAGCGGAGCAGAGCATGGTCTACTGACACT 182  
 Qy 433 SerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMet 452  
 Db 183 TCTTGTCTCCACCTGCTATGGCTCTACTCCCTGTGAGAAGCTCCACTTCTTTTATG 242  
 Qy 453 AlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGln 472  
 Db 243 GCATCAAGCATCTTCTCTCTGATCATCAAGCACCACACAGATACATGCGCACTGACCA 302  
 Qy 473 ThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSerAlaIleSerGlnLeu 492  
 Db 303 ACAATGCTAGTACAGGGCTCACCATCCCACTGATTTATCTGCAATCAGCCAACTG 362

QY 493 AlaleuGlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGlyGly 512  
 Db 363 GCTCTGGGAATTCATCCACTGTCATCTTCAGATGACAGCCGATCAAGTGCAGGTGC 422  
 QY 513 GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528  
 Db 423 GAAGATATGTCAGACACCTAGATGAATGATCTGTCGACACTCT 470

RESULT 13  
 LOCUS AL713229 510 bp mRNA linear EST 04-SEP-2003  
 DEFINITION DXFP686P1295\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
 DXFP686P1295\_5', mRNA sequence.

ACCESSION AL713229.1 GI:19696585  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 510)  
 AUTHORS Bloeker,H., Boecker,M., Brandt,P., Mewes,W., Weil,B. and  
 Wiemann,S.)  
 TITLE EST (Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B. and  
 Wiemann,S.)

JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.

No sl sequence available.  
 This clone (DXFP686P1295) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
 Location/Qualifiers  
 1..510  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DXFP686P1295"  
 /dev\_stage="adult"  
 /lab\_host="DH103"  
 /clone\_lib="686 (synonym: hlcc3)"  
 /note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiIb;  
 cDNA-collection"

## FEATURES

source

LOCUS CS18H07.y1 Human Retinal pigment epithelium/choroid cDNA  
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs18h07  
 5', mRNA sequence.

ACCESSION CA391789  
 VERSION CA391789.1 GI:24723977  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 618)  
 AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

TITLE Expressed sequence tag analysis of human RPE/choroid for the  
 NEiBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
 MEDLINE 22103460  
 PUBMED 12107410

COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 18 row: h column: 07  
 Seq primer: M3RPI reverse primer (ABI).

FEATURES  
 source  
 1..618  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

Db 102 ----- 102  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 102 ----- 102  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 102 ----- 102  
 QY 101 ValCysGlnGluAlaValTtpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 103 GTGTGTCAGGAGCAGATATGGAGACATATCGATCTTTCTGGATCGATCCCTTCACACA 162  
 QY 121 GlyGluTyrGlnAspTyrPvalSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 163 GGGGAATATCAGGACTGGGTCCAGCATCTGCAGCAGGAGACCTTCTCCCTCTTTCACATT 222  
 QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLysGln 160  
 Db 223 GGAATAACTTTCAGCAATTTCCAGGAGCACCTGGATCTTCTCCAGCAGAGAATAAACAAG 282  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 Db 283 AGAAGTTTCCCTGCACAGAAAAGATGAAATATCTGCAGAGAAGACATTTGGAGAGCCCTGGT 342  
 QY 181 -GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuTh 200  
 Db 343 TGAACCACTTGTATTTCACAGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTTCAC 402  
 QY 200 rProAspAspThrIleuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPr 220  
 Db 403 TCCTGATGACACCTCTCTCAATGAAATTTCTCGATAATATACACTCAACGACACCAAGATGCC 462  
 QY 220 oThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArg 235  
 Db 463 TACAACAGAAAGAAACAGATTTCGTTGTGGAGGAGCAGAGG 508

RESULT 14  
 LOCUS CA391789  
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs18h07  
 5', mRNA sequence.

ACCESSION CA391789  
 VERSION CA391789.1 GI:24723977  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 618)  
 AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

TITLE Expressed sequence tag analysis of human RPE/choroid for the  
 NEiBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
 MEDLINE 22103460  
 PUBMED 12107410

COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 18 row: h column: 07  
 Seq primer: M3RPI reverse primer (ABI).

FEATURES  
 source  
 1..618  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

US-10-007-270-2 (1-797) x AL713229 (1-510)

QY 1 MetTyrLeuGluThrArgAlaIlePheValPheTtpIlePheLeuGlnValGlnGly 20

Db 37 AIGTATTGGAAACATAGAGATCTATTATTGTTTTGGATTTTCTCCAAAGTTCAGGA 96

QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40

Db 97 ACCAAA----- 102

QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60

## ALIGNMENT Scores:

Pred. No.: 4,58e-65 Length: 510  
 Score: 759.00 Matches: 156  
 Percent Similarity: 66.53% Conservative: 1  
 Best Local Similarity: 66.10% Mismatches: 0  
 Query Match: 16.44% Indels: 79  
 DB: 9 Gaps: 1

/db xref="taxon:9606"  
 /clone="csl8t07"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMD108"

(Un-normalized, unamplified): cs  
 /notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp.), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp.).  
 <http://www.invitrogen.com/>". The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

## ORIGIN

Alignment Scores:  
 Pred. No.: 3,938-64 Length: 618  
 Score: 751.00 Matches: 152  
 Percent Similarity: 66.09% Conservative: 0  
 Best Local Similarity: 66.09% Mismatches: 0  
 Query Match: 18.24% Indels: 78  
 DB: 14 Gaps: 1

US-10-007-270-2 (1-797) x CA391789 (1-618)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly 20  
 DB 161 AUGTATTGGAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCAGTTCAAGGA 220  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 DB 221 ACCAAA----- 226  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60  
 DB 226 ----- 226  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 226 ----- 226  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 226 ----- 226  
 QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 227 GTGTGTCCAGGAGCAGTATGGAGAGCATATCGGATCTTCTGGATCGCATCCCTGACACA 286  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 287 GGGGAATATCAGGACTGGGTCTAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTCACATT 346  
 QY 141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
 DB 347 GGGAAAACTTCAGCAATTCACAGAGCACCCTGGATCTTCTCCAGCAGAGATATAACAG 406  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 DB 407 AGAAGTTTCCCTGCACAGAAAAGATGAATATCTGCAGAGAGACATTTGGGAGAGCTCGT 466  
 QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 DB 467 GAAACCATTTGCTATTTCACACATGTTGCCAACGCTCTACTTTGGGCCCTTCTCCCTCACT 526  
 QY 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220

Db 527 CTTGATGACACCTCTCTCATGAATTCGATATACACTCAACGACCAAGATGCCT 586  
 QY 221 ThrThrGluArgGluThrGluPheAlaVal 230  
 DB 587 AACACAGAAAGAGAAACAGAAATTCGCTGTG 616

## RESULT 15

LOCUS W26960 561 bp mRNA linear EST 08-MAY-1996  
 DEFINITION 16h10 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence.

ACCESSION W26960

VERSION W26960.1 GI:1306188

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 561)

AUTHORS Macke, J., Smallwood, P. and Nathans, J.

TITLE Adult Human Retina cDNA

JOURNAL Unpublished (1996)

COMMENT Contact: Dr. Jeremy Nathans

Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics

Johns Hopkins School of Medicine

725 North Wolfe Street, Baltimore, MD 21205

Tel: 410 955 4678

Fax: 410 614 0827

Email: jeremy.nathans@gmail.bs.jhu.edu

Clones from this library are NOT available.

PCR Primers

FORWARD: CTTTTCAGCAAGTTCAGCTCGTTAAGT

BACKWARD: GAGGTGGCTTATGATGATTCTTCACGGGTAA

Seq primer: GGGTAAAGCAAGAAAT.

## FEATURES

source Location/Qualifiers  
 1..561  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /sex="mixed (males and females)"  
 /tissue\_type="retina"  
 /dev\_stage="adult"  
 /lab\_host="E. coli strain K802"  
 /clone\_lib="Human retina cDNA randomly primed sublibrary"  
 /notes="Organ: eye; Vector: lambda gt10; Site 1: EcoRI; Site 2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library. Inserts from retina cDNA library DNA were isolated, randomly primed, PCR amplified, size-selected, and cloned into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR products were used for sequencing."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,658-63 Length: 561  
 Score: 738.00 Matches: 150  
 Percent Similarity: 93.21% Conservative: 1  
 Best Local Similarity: 92.59% Mismatches: 10  
 Query Match: 17.93% Indels: 1  
 DB: 14 Gaps: 0

US-10-007-270-2 (1-797) x W26960 (1-561)

QY 355 LeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374

DB 501 CTCANAGGCTGATCANCNAAGCACATAGGGGAGACCAATCTTTGGATGTGGGCAATT 442

QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394

DB 441 CAGTTCACTGATGAATTCGTGGATCATCTCCAGCGCTTTGGTCTTGACACCAATCAGAN 382

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QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414
Db 381 CTGCCACATCTTTGCTGTATACAGAGGATGCTACTTTGAGTCCAGAACTTCCTCT 322
QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrp 434
Db 321 GTTGAACCCAGCTTGAGACAGTGGACGGAGCAGACATGGTCTACTGACACTTCTTGG 262
QY 435 SerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSer 454
Db 261 TCTCCACCTGCTATGGCCTCTACTCTCCCTGTCCAGAACTCCACCTTCTTTATGGCATCA 202
QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474
Db 201 AGCATCTTCTCTGACTGATCAAGGCACCAAGANACATGGCCACTGACCAGACATG 142
QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494
Db 141 CTAGTACCAGGGGTCCACCATCCCAACAGTGATTATCTNCAATCAGCCCACTGGGCTCTG 82
QY 495 GlyIleSerHisProProAlaSerSerAspSerSerSerSerSerSerSerSerSer 514
Db 81 GGNATTTTCATCCACCTGCACTTTCAGATGACGNCGATCAAGTCAAGTCAAGTGGCGAATA 22
QY 514 pMet 515
Db 21 AATG 18
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Search completed: March 2, 2004, 00:40:46  
Job time : 5032 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 20:51:36 ; Search time 668 Seconds  
(without alignments)  
4304.118 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLERRAIFVFWIFLQVQ.....NSLELTVEEENHODWEGN 797

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2\_1/USPTO.spcol/US10007270/runat\_25022004\_164209\_27253/app\_query.fasta\_1.967

-DB=Published Applications NA -QWMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

-LOOPCL=0 -LOCPXT=0 -UNIT8=bits -START=1 -END=-1 -NATRX=DHMM2

-FRAN=human40.cdi LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=200000000 -USER=US10007270 @CGN 1 1 423 @runat\_25022004\_164209\_27253

-NCPUS=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.\*

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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*

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7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*

9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*

10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*

13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*

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16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	4073	98.9	3330	13	US-10-007-270-1	Sequence 1, Appli
2	4024.5	97.8	3261	13	US-10-007-270-27	Sequence 27, Appl
3	3619	97.9	2887	13	US-10-007-270-3	Sequence 3, Appli
4	3323	80.7	2244	13	US-10-007-270-5	Sequence 5, Appli
5	2548.5	61.9	3668	13	US-10-007-270-8	Sequence 8, Appli
6	1342.5	32.6	1726	13	US-10-007-270-10	Sequence 10, Appl
7	929.5	22.6	1321	13	US-10-007-270-12	Sequence 12, Appl
8	927	22.5	4166	13	US-10-007-270-16	Sequence 16, Appl
9	885	21.5	555	13	US-10-007-270-14	Sequence 14, Appl
10	846.5	20.6	2964	13	US-10-007-270-18	Sequence 18, Appl
11	841	20.4	4204	13	US-10-007-270-23	Sequence 23, Appl
12	194.5	4.7	2026	14	US-10-198-846-15589	Sequence 12589, A
13	189.5	4.6	4139	9	US-09-964-824A-105	Sequence 105, App
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17	189.5	4.6	4139	14	US-10-171-311-157	Sequence 157, App
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19	189.5	4.6	4139	15	US-10-440-464-155	Sequence 155, App
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21	188.5	4.6	1721	9	US-09-967-768A-224	Sequence 224, App
22	188.5	4.6	1721	14	US-10-097-340-211	Sequence 211, App
23	188.5	4.6	1721	14	US-10-171-311-155	Sequence 155, App
24	188.5	4.6	1721	14	US-10-007-926A-58	Sequence 58, Appl
25	188.5	4.6	1721	14	US-10-029-517-3	Sequence 3, Appli
26	188.5	4.6	2678	14	US-10-252-157-103	Sequence 103, App
27	187	4.5	2297	15	US-10-406-317-41	Sequence 41, Appl
28	185.5	4.5	1527	14	US-10-057-136-19	Sequence 19, Appl
29	183.5	4.5	1428	15	US-10-447-839A-20	Sequence 20, Appl
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33	183.5	4.5	1823	14	US-10-101-510-339	Sequence 339, App
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39	153	3.7	2166	14	US-10-282-122A-22431	Sequence 22431, A
40	149	3.6	1788	12	US-09-881-752A-165	Sequence 165, App
41	149	3.6	1888	9	US-10-240-425-1534	Sequence 1534, Ap
42	145	3.5	8224	14	US-10-177-293-89	Sequence 89, Appl
43	145	3.5	8224	14	US-10-198-846-11006	Sequence 11006, A
44	145	3.5	9647	14	US-09-880-107-3311	Sequence 3311, Ap
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#### ALIGNMENTS

RESULT 1  
US-10-007-270-1  
; Sequence 1, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 CDNA, isoform A

## US-10-007-270-1

## Alignment Scores:

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 Score: 4073.00 Matches: 796  
 Percent Similarity: 97.31% Conservative: 0  
 Best Local Similarity: 97.31% Mismatches: 1  
 Query Match: 98.93% Indels: 22  
 DB: -13 Gaps: 1

US-10-007-270-2 (1-797) x US-10-007-270-1 (1-3330)

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 QY 181 GluThrIleValIleSerThr----- 187  
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Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560
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Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720
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; Sequence 3, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2887
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform B
US-10-007-270-3

Alignment Scores:
Pred. No.: 0 Length: 2887
Score: 3619.00 Matches: 711
Percent Similarity: 90.00% Conservative: 0
Best Local Similarity: 90.00% Mismatches: 1
Query Match: 87.90% Indels: 78
DB: 13 Gaps: 1

US-10-007-270-2 (1-797) x US-10-007-270-3 (1-2887)
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Db 49 - - - - - 49
Qy 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87
Db 49 - - - - - 49
Qy 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107
Db 50 - - - - - GTGTGTCAGGAAGCAGTATGG 70
Qy 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127
Db 71 GAAGCATATCGGATCTTTCTGGATCGCATCTCTGACACAGGGGAATATCAGGACTGGGTC 130
Qy 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147
Db 131 AGCATCTGCCAGCAGAGACCTTCTGCCTCTTTGACATTGGAAAAAATTCAGCAATTC 190
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QY 168 AspGluLeuSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
DB 251 GATGAAATATCTGCAGAGAGACATTTGGAGAGCCTGGTGAAACCATTTGATTCACAA 310  
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QY 288 PheArgProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIle 307  
DB 611 TTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATC 670  
QY 308 PheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
DB 671 TTTAAGACACAGTGCAGAGCAAAAGCCCTGCAAGTGACCTCTCTCTTTTGATTC 730  
QY 328 AsnLysIleGluSerGluGluValIleHisGlyThrMetGluGluAspLysGlnProGlu 347  
DB 731 AACAAATTTGAAGTGGAGAGTGTATCATGGAACCATGGAGGAGGCAAGCAACCAAGAA 790  
QY 348 IleTyrLeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGln 367  
DB 791 ATCTATCTCAGACTACAGACTCAAGAGCTGATCAGCAAGCAGCTAGAGGAAGAACAA 850  
QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
DB 851 TCTTTGGATGTGGGACAAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCTTT 910  
QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
DB 911 GGTCTGACACCCCAATCAGAGCTGCCACATCTTTTGTGTATTAACAGAGGATGCTACT 970  
QY 408 LeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGluHis 427  
DB 971 TTGAGTCAGAACTTCTCTCTGTTGAACCCAGCTTGAGACAGTGGAGCGGACAGCAT 1030  
QY 428 GlyLeuProAspThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGluAla 447  
DB 1031 GGTCTACCTGACATCTTGTGTCTCCACCTGCTATGAGCTCTACCTCCCTGTGAGAGCT 1090  
QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
DB 1091 CCACCTTTCTTATGGCATCAAGCATCTCTCTGACTGATCAGGACCAACAGATACA 1150  
QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
DB 1151 ATGGCCACTGACAGACAATCTAGTACAGGCTCACCATCCCACTGATGATTTCT 1210  
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArg 507  
DB 1211 CCAATCAGCCCACTGGCTCTGGGAATTTACATCCACTGATCTTCAGATGACAGCCGA 1270

QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
DB 1271 TCAAGTGCAGGTGGCAAGATATGGTGCAGACCTAGATGAAATGGATCTGTGTGACACT 1330  
QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
DB 1331 CTTGCCCATCTCAGGTACCAAGGCTCAGGGAATAGCTTTCTGTCACAGATCAATTTCTTG 1390  
QY 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567  
DB 1391 GAGGATACCACTCTCTCAGCTTACAGTATATCACCAGTATGTTCTATGACCATTTGCC 1450  
QY 568 ProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
DB 1451 CCCAAGGCGAGAGCTGTAGTGTTCCTCAGTCTCGGTGTTGCTTAACATGGCTTTCTCC 1510  
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
DB 1511 AACGACCTGTCAACCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAG 1570  
QY 608 LeuLeuValProTyrLeuArgSerLeuThrGlyPheLysGlnLeuGluLeuLeuAsn 527  
DB 1571 CTCTCTGGTTCCATATCTACGATCCCAATCTTACAGGATTTTAAAGCAACTTGAAATACTTAAC 1630  
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
DB 1631 TTCAGAAACCGGAGTGTGATTGTGAATACAAATGAAGTTTGTCTAAGTCTGTGCGGTAT 1690  
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667  
DB 1691 AACCTCACCAAGGCTGTGCACGGGTCTTTGGAGGATTTTCTGTTCTGTCAGCCCAACAA 1750  
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
DB 1751 CTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAACAGATCCC 1810  
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707  
DB 1811 TGCAAGTCTCTGGCTGGCGCAATTTGCCAATGTGTAAAGAACGAAACGACTGAGGAA 1870  
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727  
DB 1871 GGGAGTGTCTGCTGAAACAGGATATGACCCAGGAGGAGCTGGAGCTGTGAAACCA 1930  
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747  
DB 1931 GGCCTCTGTGGCCCTGGCACAAAGGAATGCGAGGTCTCCAGGAAAGGAGCTCCATGC 1990  
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767  
DB 1991 AGGTTGCCAGATCACTCTGAAATCAAGCATACAAACACTAGTGTATAAAGATTCACAAAT 2050  
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787  
DB 2051 CAACAAATAACAAGTAATCAGTAAAGAAATTTCTGAATTACTGACCGGTAGATATGAA 2110  
QY 788 GluPheAsnHisGlnAspTyrGluLysAsn 797  
DB 2111 GAATTTAACCATCAAGATTGGGAGGAAAT 2140

## RESULT 4

US-10-007-270-5  
; Sequence 5, Application US/10007270  
; Publication NO. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195

; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 2244  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(2244)  
 ; OTHER INFORMATION: n is a, c, g, or t.  
 US-10-007-270-5

Alignment Scores:  
 Pred. No.: 0 Length: 2244  
 Score: 3323.00 Matches: 667  
 Percent Similarity: 95.56% Conservative: 0  
 Best Local Similarity: 95.56% Mismatches: 10  
 Query Match: 80.71% Indels: 23  
 DB: 13 Gaps: 1

US-10-007-270-2 (1-797) x US-10-007-270-5 (1-2244)

QY 1 MetTyrLeuGluThrArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly 20  
 DB 151 ATGTATTGGAACTAGAGAGCTATTGTTGTTTTTGGATTTTCTCCAAAGTTCAAGGA 210  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro 40  
 DB 211 ACCAAAGATATCCATTAAACATATACCATCTGAAACTTAAGACATAGACATNCCCA 270  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 DB 271 AGAATGAACAACTGAAAGTACTGAAATAATGTACAAATGTCAAAATGTCAACTATGAGACGAATA 330  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 331 TTCGATTGGCAAGNATCGAACAAAGATCCGATTTTCCCAACGGGGTTAAAGTC 390  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 391 TGTCACAGGAATCCATGAACACAGATTTTAGACAGCTCTTCAAGCTTATTATAGATTGAGA 450  
 QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 451 GTGTGTCCAGAGAGCATGGGAACATATCGGATCTTTCTGGATCGCATCCCTGACACA 510  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 511 GGGGAATATCAGAGCTGGGTGACGATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATT 570  
 QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleIleGln 160  
 DB 571 GGAAAAAATTCAGCAATTCAGAGACCTGGATCTTCTCCAGCAGAGAATAAAGACAG 630  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 DB 631 AGAAGTTCCTGTGACAGAAAGATGAATATCTGCAGAGAGACATTGGGAGAGCCTGGT 690  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 691 GAACCAATTGCTATTCAAC-AGCAATCTACATTTCAAGACTGGGCGAGTATTCTAAGA 749  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 750 AAACCTCAGAGAGCAATTCAGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTC 809  
 QY 200 ThrProAspAspThrLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219

DB 810 ACTCTGATGACACCCCTCCTCAATGGAATTTCTCGAATAATACACTCAACGACACCAAGATG 869  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValIleGluGlnArgValGluLeuSer 239  
 DB 870 CTTACACAGAGAAAGAGAAACAGAAATTCGCTGTGTGGAGGAGCAGAGGTGGAGCTCAGC 929  
 QY 240 ValSerLeuValAenGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
 DB 930 GTCTCTCTGTGTAAACCAAGAGTTCAAGGACAGAGCTGCTGACTCCAGTCCCATATATAC 989  
 QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
 DB 990 CAGGAGCTAGCAGAAAGTCCCACTTCAGATCCAAAGATATTTAAGAACTTCCAGGA 1049  
 QY 280 PheLysLysIleHisValLeuGlyPheArgProLysGlyLysAspGlySerSerSer 299  
 DB 1050 TTCAAAAAAATCCATGTGTTAGGATTTAGACCAAGAAAGAAAGATGCTCAAGCTCC 1109  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 DB 1110 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCAGAAAGCAAAAGCCCTGCA 1169  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339  
 DB 1170 AGTGACCTCTGCTTTTGTATCCAAACAAATTTGAAAGTGAGGAAGTCTATCATGGAACC 1229  
 QY 340 MetGluLysAspLysGlnProGluIleTyrLeuThrAlaThrAspLysArgLeuIle 359  
 DB 1230 ATGGAGAGACAAAGCAACAGAAATCTATCTCACAGCTACAGACCTCAAAAGCGTGATC 1289  
 QY 360 SerLysAlaLeuGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
 DB 1290 AGCAAGCACTAGAGAGAGACAAATCTTTGGATGTGGGACAAATTCAGTTCACTGATGAA 1349  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 DB 1350 ATTGCTGGATCACTGCCAGCCTTTGCTCTGCTCACCCCAATTCAGAGTGCCCACTTTT 1409  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeu 419  
 DB 1410 GCTGTTATAACAGAGATGCTACTTTGAGTCAGAACTTCTCTCTGTTGAAACCCAGCTT 1469  
 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMet 439  
 DB 1470 GAGACAGTGGACGAGCAGAGATGCTTACCTGACACTTCTTGGTCTCCACCTGCTATG 1529  
 QY 440 AlaSerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeu 459  
 DB 1530 GCCTT-ACCTTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTCG 1588  
 QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1589 ACTGATCAAGGCACACACAGATACAAATGGCCACTGACCCAGACAAATGCTAGTACCAGGGCTC 1648  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
 DB 1649 ACCATCCCAACAGATGATTATTCTGCAATCAGCCAACTGGCTCTGGGAATTTCAATCCA 1708  
 QY 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
 DB 1709 CTTGATCTTCAGATGACAGCCGATCAAGTCAGGTGGCGAAGGTATGGACAGACCTTA 1768  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
 DB 1769 GATGAATGGATCTGTCTGACACTCTGCCCCACTCTGAGGTACCAAGCTCAGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
 DB 1829 GTTCTGTCTCCAGATCAATTTCTTGAGGATACCACTCTCTGTCTGAGTTTACAGTATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeu 579  
 DB 1889 ACCACTAGTTCTATGACCAATTCGCCCAAGGCCGAGAGCTGGTAGTGTCTTCTCAGTCTG 1948

QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
 Db 1949 CGTGTGCTAAACATGGGCTTCTCCACAGCCTGTTCACAAAGACTATTGGAGTACCGA 2008  
 QY 600 AlaLeuGluGlnGlnPheThrGlnLeuValProTyrLeuArgSerAsnLeuThrGly 619  
 Db 2009 GCTCTGGAGCAACAATTACACAGCTCTGTGTCATATCTACGTCCTTACAGCA 2068  
 QY 620 PheLysGlnLeuGluLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
 Db 2069 TTTAAGCAACTTGAATACTTAACTTCAGAAACGGAGTGTGATTGTGAATAGCAAAATG 2128  
 QY 640 LysPheAlaLysSerValProTyrAsnLeuThrIleValIleValIleValIleVal 659  
 Db 2129 AAGTTTGTCTAAGTCTGCTGCGTATTAACCTCACCAGGCTGTGCACGGGCTTTGGAGGAT 2188  
 QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677  
 Db 2189 TTTCTGTTCTGTCAGGCCCAACCACTCCATCTCGAAATAGACAGCTACTCTCTC 2242

## RESULT 5

US-10-007-270-8  
 ; Sequence 8, Application US/10007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hageman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007,270  
 ; CURRENT FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 3668  
 ; TYPE: DNA  
 ; ORGANISM: Mus sp.  
 ; FEATURE:  
 ; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform A  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(3668)  
 ; OTHER INFORMATION: n is a, c, g, or t.  
 US-10-007-270-8

## Alignment Scores:

Pred. No.: 5,38e-260 Length: 3668  
 Score: 2548.50 Matches: 528  
 Percent Similarity: 75.12% Conservative: 79  
 Best Local Similarity: 65.35% Mismatches: 180  
 Query Match: 61.90% Indels: 21  
 DB: 13 Gaps: 9

US-10-007-270-2 (1-797) x US-10-007-270-8 (1-3668)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 Db 196 ATGAATTTTCAAAATAAAGATGCTATCTTTGTTTGGGATTTTCTCCAAAGTTCAAGGA 255  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro 40  
 Db 256 ATCAAGATACCTCTATTAAATATTTCAGTTCTGTAATTAATAACATAGACAAACCCCA 315  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrValArgArgIle 60  
 Db 316 AGAATCGAAACAATTAAGAGTACTTCAACAGTGCACAAAGTGTCAACCATGAACGATA 375

QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 376 TTCGATTTCGCAAGCTTCGAACCAAAAGATCAGCACTTTTCCCA---GCTGCTAAATC 432  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 433 TGCCACAGGAATCCTTGAGACAGATTTTAGCAAGTCTTCAAGAAATATTATATAGCTGAGA 492  
 QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 493 GTATGTCAAGAGTCGTGTGGGAAGCATATCGTATCTTTCTGGACCGAATTCCTGCACACA 552  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 553 GAGGAATATCAGACTGGGTTCAGCTCTGCCAAGAAAGAAACCTTCTGCTCTTTTGACATT 612  
 QY 141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
 Db 613 GGGAAAAAATTCAGCAACTCCAGGAGCACCTAGATCTTCTTCAGCAGAGAAATAAAACAG 672  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluProGly 180  
 Db 673 AGAAGCTTCTCTGGAGGAAGATGAGACAGCTCCATGGAGACACTGGAGCACCTACT 732  
 QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 733 GAAGCCCTGTGTACCCACAGATGTTTCCAGGATGTCTCTGGGCGCTTCCCACTTCT 792  
 QY 201 ProAspAspThrLeuAsnGlnIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 Db 793 TCGATGACACAGACCTCAAGGAGATTCCTCAGTGTCCCTCAGGACATTCACCAAGGCC 852  
 QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGln 234  
 Db 853 ACAACAGAAAGTAAACAGAACCTATTACGCTGTCTGAATTTCTCA-----TCAGAGGAG 906  
 QY 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
 Db 907 AAGTGGAAATTGAGCATCTCTGCCAAACACACAGGTCAGGTCAGGCGAGAGCTCACCACCT 966  
 QY 255 GlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
 Db 967 GGGTCACCATACTACCAAGAACTGGTGGGACAGTCCCAACTGCAGTTGCCAAAGATATT 1026  
 QY 275 LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
 Db 1027 AAGAAACTTCCAGGATTCGGAGAAATCCGTGTATTAGGATTTAGACCACAAAGAAAGAA 1086  
 QY 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
 Db 1087 GATGGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGGACCATGCAGAA 1146  
 QY 315 AlaLysSerProAlaSerAspLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
 Db 1147 GCAAAAGCCCTGATAGTCATCTCTGTGTTTCCAAACAAATTTGAAAGTGAAGA 1206  
 QY 335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAsp 354  
 Db 1207 ATCCATCATGGAGTCATA--GAACACAAACACACAGAAACCTACCTCACAGCTACAGAC 1263  
 QY 355 LeuLysArgLeuLysSerLysAlaLeuGluGlnGlnSerLeuAspValGlyThrIle 374  
 Db 1264 CTCAAAAAATCATCATCAACTACTAGTAGAGACCTGCTCTCTGGTAGAAGGGGAAATTT 1323  
 QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
 Db 1324 CCATTCCGGTGAAGTACTGGGACACTC-----TTCAGACCTGTCTCACTGAACCATGAT 1377  
 QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
 Db 1378 CTGCCCAAGCCCTGCTGATGATGCAGAGGATGCCACTTTGAGTCCAGAACTTCCTTC 1437  
 QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430

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Db 1438 GTTGAGCTTAGGCTTGAGGAGTGAGCAGAGAGATCTGAGCTGCCTGGAAATGCTCTCC 1497
QY 431 ---AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449
Db 1498 AAAGACAGTCTTGCTGCTCCACCTGTATCAGCCTCAATTTCCCGATCAGAAAATCTACCT 1557
QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
Db 1558 TCGTTT---ACACCTAGATCTTCTCTAGATGCTCAAGCCCTCCCTCGATGACC 1614
QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSerAlaIle 489
Db 1615 ACTGCCCAACAGCACTCATCCCAAGCCCACTCTCCCACTACTCGATTATCTACCATC 1674
QY 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSer 509
Db 1675 CGCCAATTGCTCTGGAATCTGCAATTCGCTGCTGCTCCATGTCAGACAGAGCTGATC 1734
QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
Db 1735 ACAACGACCATGACACAACTCGAGACCTAGATGGCATGGATGTCTGACACGCCAGCC 1794
QY 530 ProSerGluValProGluLeuSerGluTrpValSerValProAspHisPheLeuGluAsp 549
Db 1795 TTGTCAGAAATATCAGAACTCAGTGGATACGATTCTGCTCGGGTCAGTTCTTGAGATG 1854
QY 550 ThrThrProValSerAlaLeuGlnTrpIleThrThrSerSerMetThrIleAlaProLys 569
Db 1855 ACCACACCCATCCCAACAGTAGGTTCATCCACCAGCTCCGAGACCATGTCACCAAG 1914
QY 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589
Db 1915 GCGCAGGAGCTAGTGGTATTCTTACGCTGGCTGTGTAACTAAGTCCGCTTCTCTATGAC 1974
QY 590 LeuPheAsnLysSerSerLeuGluTrpArgAlaLeuGlnGlnPheThrGlnLeu 609
Db 1975 CTGTTCAACAGAGTCTCTGGAGTATCAGCCCTGGAAACCAACGATTCACAGACCTGCT 2034
QY 610 ValProTrpLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629
Db 2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCACTGGAATATCTCAGCTTCAGA 2094
QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTrpAsnLeu 649
Db 2095 AACCGAAGTGTATCGTGAACAGCAAGTGGGTTCGAAAGGGGGTACCCCTACAACCTC 2154
QY 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669
Db 2155 ACCCAGCGCTGCGGGGTCTTGAGGATCTTCGTCACCGCAGCTCAAGGCTCAAT 2214
QY 670 LeuGluIleAspSerTrpSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
Db 2215 CTGGAATCGAAAGCTACTCCCTCAGCATTTGAACAGCTGATCAGCGGATCCCTGCAAA 2274
QY 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709
Db 2275 CTCCTAGACTGGCAAAATTTCCCAAGTGTGTAAAGAATGAGTCGACAGAGAGCAGAG 2334
QY 710 CysArgCysLysProGlyTrpAspSerGlnIleSerLeuAspGlyLeuGluProGlyLeu 729
Db 2335 TGTCTGTCGACAGAGGACATGAGACCAAGGACCTCGGACTACCAAGCCCTCAAGCCCTC 2394
QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749
Db 2395 TGTCCCTCTGGA---AAGACTTGTGGCGCGCCGAGAACCAAGCACTCCATGACGCCA 2451
QY 750 ProAspHisSerGluAsnGlnAlaTrpLysThrSerValLysPhePheGlnAsnGln 769
Db 2452 CCAGATCACTACAAACCAAGCTCAGGAACCTGGTGTAAAGCTA-----CGTCAG 2505
QY 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuThrValGluTrpGluGluPhe 789
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Db 2506 CAAATAAGGTAGTCAAGAAAAGAAATTTAAACTATCAGCTATAGGATTTGAAGAATTT 2565
QY 790 AsnHisGlnAspTrpGluGlyAsn 797
Db 2566 GAAGACAGGAGCTGGAGGGAAT 2589
RESULT 6
US-10-007-270-10
; Sequence 10, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D
US-10-007-270-10
Alignment Scores:
Pred. No.: 2,89e-132 Length: 1726
Score: 1342.50 Matches: 310
Percent Similarity: 44.96% Conservative: 51
Best Local Similarity: 38.61% Mismatches: 99
Query Match: 32.61% Indels: 343
DB: 13 Gaps: 9
US-10-007-270-2 (1-797) x US-10-007-270-10 (1-1726)
QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly 20
Db 140 ATGAATTTCAATTAACATGCTATCTTTTGGGATTTTCTCCAGTTTCAGGA 199
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Db 199 ----- 199
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60
Db 199 ----- 199
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
Db 199 ----- 199
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db 200 -----ATCAA 205
QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db 206 GTATGTCAGAGAGTCGTGGGAGCATATCGTATCTTTGGACCGAATTCCTGACACA 265
QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
Db 266 GAGGAATATCAAGACTGGGTGAGCTCTGCCAAGAAACCTCTGCTCTCTTGCATT 325
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160
Db 326 GGGAAAAACTTCAGCACTCCCGAGGACCTAGATCTTCTTCAGCAGAGATAAAGACAG 385
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161 ArgSerPheProAspArgLeuLeuSerAlaGluLysThrLeuGlyGluProGly 180  
1177  
386 AGAAGCTTCCTGGGAAAGATGACACAGCCCTCCATGGAGCACCTGAGCACCTACT 445  
181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
1177  
446 GAAGCCCTGTGGTACACACAGATGTTCCAGGATGTCCTGGGGCCATTCCCACTCTCT 505  
201 ProAspThrLeuLeuAsnGluLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
1177  
506 TCTGATGACACAGACCTCAAGGAGATTCTCAGTGTCACTCCCTCAAGGACATTCACCAAGCCC 565  
221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234  
1177  
566 ACAACAGAAAGTATAACAGAACCTATTTCAGTGTCTGATTTCTCA-----TCAGAGGAG 619  
235 ArgValGluLeuSerValSerLeuValAlaGlnLysPheLysAlaGluLeuAlaAspSer 254  
1177  
620 AAGGTGGAGTTACAGCATCTCTCTGCCAAACACACAGGTTCAAGGCAGAGCTCACCAACTCT 679  
255 GlnSerProTyrThrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
1177  
680 GGGTCACACTACCAAGAACTGGTGGACAGTCCCACTGAGTTGCAAAAGATATT 739  
275 LysLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
1177  
740 AAGAACTTCAGGATTCGGGAAATCCGTTATTAGATTAGACCAAGAAAGAGAA 799  
295 AspGlySerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
1177  
800 GATGGTTCAAGCTCCACAGAAATACACTTATGGCCATCTTAAAGAGGGACCATGTCAGAA 859  
315 AlalysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
1177  
860 GCAAAAGCCCTGATGATCTACTGCTCTGTGATTCACACAAATTTGAAAGTGAAGA 919  
335 ValTyrHisGlyThrMetGluGluAspGlyGlnProGluIleTyrLeuThrAlaThrAsp 354  
1177  
920 ATCCATCATGGAGTCATA---GAAGCAAAACACCAAGAACTACCTCACAGCTACAGAC 976  
355 LeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374  
1177  
977 CTCAAAATCATCATCACTACTGATGAGAGACCTGCTTGTAGAGGGAATAAT 1036  
375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
1177  
1037 CCATTGGTGATGAAGTTACTGGACACTC---TTACAGCCTGTCTCACTGAACCAT 1090  
395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
1177  
1091 CTGCCCCAAGCCCTTGTGATGTCACAGAGGATGCCACTTTGATGCCAGAACTTCTTTTC 1150  
415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyr 434  
1177  
1151 GTTGAGCTAGGCTTGAGGAGTGGAC----- 1177  
435 SerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSer 454  
1177  
455 SerIlePheSerLeuThrAspGlnGlyThrAspThrMetAlaThrAspGlnThrMet 474  
1177  
475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
1177  
495 GlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGlyGlyGluAsp 514  
1177

515 MetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValPro 534  
1177  
535 GluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThrProValSer 554  
1177  
555 AlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuVal 574  
1177  
575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSer 594  
1177  
595 SerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArg 614  
1177  
615 SerAsnLeuThrGlyPheLysGlnLeuGluLeuAsnPheArgAsnGlySerValIle 634  
1178  
635 ValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHis 654  
1195  
655 GlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluLeuAspSer 674  
1195  
675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGly 694  
1196  
695 GluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysPro 714  
1238  
1238 AAATTGTCCTGAGTGTGTAAGAAATGAGTGGACAGAGGAAGCAGAGTGTGCTGTCAGACAG 1297  
715 GlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThr 734  
1298  
1298 GGACATGAGAGCCAGGAGCCCTGACCTACAGACCCCTGAACCTCTGTCCCTCTGGA--- 1354  
735 LysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlu 754  
1355  
1355 AAGACTTGTGGCGCGCCGAGAAACAAGCAACTCCATGCGAGGCCACAGATCACTCTACA 1414  
755 AsnGlnAlaTyrLysThrSerValLysPheGlnAsnGlnGlnAsnAsnLysValIle 774  
1415  
1415 AACCAAGCTCAGGAACCTGGTGTAAAGGCTA-----CGTCAGCAAAATAAGGTAGTC 1468  
775 SerLysArgAsnSerGluLeuThrValGluTyrGluGluPheAsnHisGlnAspTyr 794  
1469  
1469 AAGAAAGAAATTTAAACTATCAGCTATGAGTATTGAAGATTTGAAGACCAAGGACTGG 1528  
795 GluGlyAsn 797  
1529  
1529 GAGGGAAT 1537

## RESULT 7

US-10-007-270-12  
; Sequence 12, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195

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; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform E
US-10-007-270-12
Alignment Scores:
Pred. No.: 1.57e-88 Length: 1321
Score: 929.50 Matches: 185
Percent Similarity: 79.41% Conservative: 31
Best Local Similarity: 68.01% Mismatches: 53
Query Match: 22.58% Indels: 3
DB: 13 Gaps: 2
US-10-007-270-2 (1-797) x US-10-007-270-12 (1-1321)
QY 526 AspThrProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHis 545
DB 320 GAAAGCCAGCCTTGTGAGAAATATACAGACTGATGATACGATTCGCTCGGGTCAG 379
QY 546 PheLeuGluAspThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThr 565
DB 380 TTCCTTGAGATGACACACACCATCCACAGTACGGTTCATCACACAGCTCCGAGCC 439
QY 566 IleAlaProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAla 585
DB 440 ATTGCCACCAAGGCGCAGGAGTAGTGTATTCTTCAGCTGCGTGTGTTAATCATGCCG 499
QY 586 PheSerAsnAspLeuPheAsnLysSerSerLeuGlnTyrArgAlaLeuGluGlnPhe 605
DB 500 TTCCTCTATGACCTTTCAACAAGAGTCTCTGGAGTATCAAGCCCTGGAAACACAGATC 559
QY 606 ThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluLe 625
DB 560 ACAGACCTGCTGTTCCCTATCWCAGATCGAATCTTACGGGATTAAGCACTGGAATA 619
QY 626 LeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerVal 645
DB 620 CTCAGCTTCAGAAACGGAAGTGTGATCGTGAACAGCAAAAGTGGCGTTTGCAAGGCGGTA 679
QY 646 ProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaAla 665
DB 680 CCTTACACCTCACCAGGCGCGTGGCGGGTCTTGGAGGATCTTCGGTCCACCGCAGCT 739
QY 666 GlnGlnLeuHisLeuGluLeuAspSerTyrSerLeuAsnIleGluProAlaAspGlnAla 685
DB 740 CAAGGCTCAATCTGGAAATCGAAAGTACTCCCTCGACATTTGAACACGATGATCAGCGC 799
QY 686 AspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThr 705
DB 800 GATCCCTGCAAACTTCTAGACTGTGCAAAATTTGCCAGTGTGTAAGAATAGTGGACA 859
QY 706 GluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeu 725
DB 860 GAGGAAGCAGAGTGTGCTGCAGACAGGCGACATGAGCGCACCGGACCTCGACTTACCAG 919
QY 726 GluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAla 745
DB 920 ACCCTGAACCTGTGCTCCCTCGA---AAGATTGTGTGGCGCGCGAGAACCAAGCAACT 976
QY 746 ProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPhe 765
DB 977 CCATGAGGCCACCATCCTACAAACACCAAGCTCAGAACTGGTGTAAAGGCTA 1036
QY 766 GlnAsnGlnGlnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGlu 785
DB 806 AATTGTGTGAGGATGAGTGCACAGATATATTGAAATGGGCACAAATTTTAGTGAATCT 865
;
Db 1037 -----CGTCAGCAAAATAAGTGTAGTCAAGAAACGAAATTTCTAAACTATCAGCTATAGCA 1090
QY 786 TyrGluGluPheAsnHisGlnAspTTPGluGlyAsn 797
DB 1091 TTTGAAAAATTGAAAGACACGAGACTGGGAGGAAAT 1126
RESULT 8
US-10-007-270-16
; Sequence 16, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 4166
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IPM 200 (isoform A) cDNA
US-10-007-270-16
Alignment Scores:
Pred. No.: 1.82e-87 Length: 4166
Score: 927.00 Matches: 297
Percent Similarity: 39.71% Conservative: 145
Best Local Similarity: 26.68% Mismatches: 267
Query Match: 22.52% Indels: 405
DB: 13 Gaps: 36
US-10-007-270-2 (1-797) x US-10-007-270-16 (1-4166)
QY 2 TyrLeuGluThrArgArgAlaIlePheValPheThrIlePheLeuGlnValGlnGlyThr 21
DB 202 TTCCTCTTTTGGAGAGATTTCTTGGGTATTTTG-ATATTTGCTGTAGTAGAGAGAC 260
QY 22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39
DB 261 TTTCCATCATTAACAGCAAAACCTACTTATCT---ATAGAGGAGATCCAGAACCCCAAG 317
QY 40 -----ProArgAsnGluThr-----ThrGluSer 47
DB 318 AGTGCAAGTTTCTTTCTCTGCTGCTGAGAAATCAACAGACCTTCTCTAGTACCAAAAG 377
QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67
DB 378 AAACAGCCTCTGCGACCGCAGAGAAACTGAAAGACAGTGGTTA-----ATCAGA 425
QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGlnSerMetLys 87
DB 426 AGCGGAGATCTATTCTGTTTCTTAATGAGTGAATAATCTGCCAGATGAAGTGTGCA 485
QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTyr 107
DB 486 GAGGCTGTGCAAAATCATGTGAGTATTTTAAAGTCGAGTGTGTGAGGAGTGTCTCG 545
QY 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrVal 127
DB 546 GAAGCCTTCAGGACTTTTGGGATCGACTCTCTGGCGGTGAGGAATATCATCTACTGATG 605
QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147
DB 606 AATTGTGTGAGGATGAGTGCACAGATATATTGAAATGGGCACAAATTTTAGTGAATCT 665

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Qy	397	-----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro	410
Db	1659	ACCCGCGCAGTGTCTCAGACTGGCTTGGCTTCTCGAGAAAGGACTTCTGGATCT	1718
Qy	411	GluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlu	426
Db	1719	CACCTTG-----GTAGAAGATGATTAGCCATGTTGAAGAGTCAGAAGATTTCCTTCT	1772
Qy	427	---HisGlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThr	442
Db	1773	ATTGATTCAATTCCTTCAGATTCAATCACTCACTCACTGTGCCAAAAGAAACAATACCATCC	1832
Qy	443	-----SerLeuSerGluAlaPro	450
Db	1833	ATGGAAGACTCTGATGTGCTTACCATCTTACCATATCTGCCTTCCTATACCTTTT	1892
Qy	451	PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr	470
Db	1893	GGCTTGGACTCCTTGACCTCCAAAGTCAAAGACCAATTAAAGTAGCGCTTTCCTCGCCA	1952
Qy	471	AspGlnThrMet	474
Db	1953	GATGCAATCCATGGAAAGAGTTAATATTGACGGTGGTTTAGTTTCAGGCTGGGCAA	2012
Qy	475	LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu	494
Db	2013	AAGGTAGATCTGATTACTTGGCCATGAGTGAGACTTCATCA--CAGAAGAGCGCGAA	2069
Qy	495	GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAsp	514
Db	2070	CCACTGTCCAAAGCGGTGTGAAGATGATGATCTCACTTTGCCAGCTGAGATTGAAGAC	2129
Qy	515	MetValArgHisLeu---AspGluMetAspLeuSerAsp	526
Db	2130	AAGAACTAGTTTACTTGACAAATGGATCCACAGACCAATTAGTAAGCACTCAAAA	2189
Qy	527	-----ThrProAlaProSerGluValPro	534
Db	2190	TATGAACATGATGACAGATCCACACACTTTCAGAGGAAGAGCGCTTATAGTGGCGCTGCT	2249
Qy	535	-----GluLeuSerGluTyrValSerValProAspHisPhe	546
Db	2250	GTGCCATCTTCGACATACTGCAGCTGATCTGCGTCTCTAACCTCCCAAGCACATA	2309
Qy	547	LeuGlu	550
Db	2310	TCAGAAGTACCTGGTGTGATGATTGCTCAGTTACCAAGACACCTCTTATCTGACATCT	2369
Qy	551	ThrProValSerAla	555
Db	2370	GTAGCAATCTCTGCCCTCTACTGATAAATCAGATCAGGCAGATGCCATCTTAAGGGAGGAT	2429
Qy	556	LeuGlnTyrIleThrThrSerSer	563
Db	2430	ATGGAACAAATTACTGATGATCCCACTATGAATGTTTGACAGTGAGGTTTCAATGGTA	2489
Qy	564	-----MetThrIleAlaProLysGlyValGlu	572
Db	2490	AAGCCAGATATGCAAACTTTGTGGACTATATTGCCAGAAATCAGAGAGAGTTTGGACAAGA	2549
Qy	572	-----	572
Db	2550	ACTTCTTCCCTAGAGAAATTGTCAGAGACATATTGGCAAGTACACCACAGAGTGCTGAC	2609
Qy	572	-----	572
Db	2610	AGGCTCTGGTTATCTGTGACAGACTTACCAAATTTGCCCTCCCAACCACAAATCTCCACCTTG	2669
Qy	572	-----	572
Db	2670	CTAGAGATGAAGTAATTATGGGTGTACAGGATATTTCGTTAGAACTGGACCGGATAGCC	2729
Qy	572	-----	572



Db 2730 ACAGATTACTATACGCTGACGAACTCCAGAGCAAAATGGCAAGGTGGTATGTTAGTG 2789  
Qy 572 ----- 572  
Db 2790 GAAATGTCAACAGTGTTCACCTCCACAGAGATGGTTAGTGGCTTGGCCACAGAGGA 2849  
Qy 573 -----LeuValValPhePheSerLeuArg 580  
Db 2850 GGAGATGACTTGAGTTATACCAGACTTCAGAGCTTTGGTGGTTTCTTCAGCCCTCCGA 2909  
Qy 581 ValAlaAsnMetAlaPheSerAsnLeuPheAsnLysSerLeuGluTyrArgAla 600  
Db 2910 GTGACTACATGATGTTTTCAGAGACTGTTTAAATAAACAACCTCTGGAGTATAAGCC 2969  
Qy 601 LeuGluGlnPheThrGlnLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 2970 CTGAGCAAGATTCCTAGAAATCTGCTGTTCCCTATCTCCAGTCAAAATCTCAGGGGTT 3029  
Qy 621 LysGlnLeuGluLeuLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 3030 CAGAACTTAGAATCTCACTTCAGAAATGGCAGCAATTTGGTGAACATCGAATGAAG 3089  
Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
Db 3090 TTTGCCAATCTGCTCCCTTACAGTCAACAATCGCGGTGTACATGATCTCGAAGACTTT 3149  
Qy 661 ArgSerAlaAlaGlnLeuHisLeuGluLeuAspSerTyrSerLeuAsnIleGlu 680  
Db 3150 TGTACCATGCTCAATACCATGAACTGGCTATGTAATAACTCTCTTGATGGGAA 3209  
Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
Db 3210 TCAGTGTAGTGAAGCAACCTTCAAGTTTCAGGCTGTAATGAATTTTCAGAGTGTCTG 3269  
Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719  
Db 3270 GTCAACCCCTGGAGTGGAGAGCAAGTGCAGATGCTTCCCTGGATACCTGAGTGTGAA 3329  
Qy 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735  
Db 3330 GAACGGCCCTCTCAGAGTCTCTGTACCTACAGCTGACCTGCTGCTGATGATGGAAG 3389  
Qy 736 GluCysGluValLeuGlnGlyLysGlyAlaProCysArg 748  
Db 3390 ---TGTGACATTATGCTGGCGACGGGCCATTTGTAGG 3425

RESULT 9

US-10-007-270-14  
; Sequence 14, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Monkey IPM 150 cDNA (partial)  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Monkey species

US-10-007-270-14

Alignment Scores:  
Pred. No.: 2,12e-84 Length: 555  
Score: 885.00 Matches: 167  
Percent Similarity: 95.65% Conservative: 9  
Best Local Similarity: 90.76% Mismatches: 8  
Query Match: 21.50% Indels: 0  
DB: 13 Gaps: 0

US-10-007-270-2 (1-797) x US-10-007-270-14 (1-555)

Qy 73 PhePheProThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSer 92  
Db 4 TTTCTTCCGACGGGGTTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTAGCCAGT 63  
Qy 93 LeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTyrGluAlaTyrArgIle 112  
Db 64 CTTCAAGCTTTATTATAGATTGAGAGTGTGTGAGAAAGCAGTATGGAAAGCATATCGGATC 123  
Qy 113 PheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrValSerIleCysGlnGln 132  
Db 124 TTTCTGGATCGCATCCCTGTGACACAGGGGAATATCAGGACTGGTTCAGCTTCTGCCAGCAG 183  
Qy 133 GluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSerGlnGluHisLeuAsp 152  
Db 184 GAGACCTTCTGCTCTTTGACATCGACACAAACTTCAGCAATTCAGGAGCAGCCTGGAT 243  
Qy 153 LeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAla 172  
Db 244 CTTCTCCAGCAGAGAAATAAACAGAGAAGTTTCCCTGAGAGAAAGATGAAGTATCTACA 303  
Qy 173 GluLysThrLeuGlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnVal 192  
Db 304 GAGAAGACATTTGGGAGAGCTAGTGAACCATTTGTGGTTTCAACAGATGTTGCCAGCCTC 363  
Qy 193 SerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsn 212  
Db 364 TCACCTGGGCTTTCCCTGCTACTCCTGATGACACCTCCTCAATGAATTTCTCGATTAAT 423  
Qy 213 ThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGlu 232  
Db 424 GCATCAACGACACCAAGATGCTTACACAGAGAAAGAGAAACAGAACTCGCTGTGTCTGAG 483  
Qy 233 GluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAla 252  
Db 484 GAGCAGAGGGTGGAGCTCAGCATCTCTCTGATAAACCAAGAGGTTTCAGGCGAGAGCTCGCT 543  
Qy 253 AspSerGlnSer 256  
Db 544 GACTCTCAGTCA 555

RESULT 10

US-10-007-270-18  
; Sequence 18, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 2964  
; TYPE: DNA



QY 531 -----SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGlu 548  
Db 1964 CACATATCAGAGTACCTGGTGTGATGATTAAGTACAGTACCAAGACCCCTTATATCTG 2023  
QY 549 AspThrProValSerAla  
Db 2024 ACATCTGTAGCAATCTGCTCTACTGATAAATCAGATCAGCAGATGCCATCCTAAGG 2083  
QY 556 -----LeuGlnTyrIleThrThrSerSer  
Db 2084 GAGGATATGGAAACAAATTAAGTACGATCCCACTATGATGATGATGATGATGATGATGAT 2143  
QY 564 -----MetThrIleAlaProLysGlyArgGlu  
Db 2144 ATGGTAAGCCAGATATGCAAACTTTGGGACTATATGGCAGATCAGAGAGTTGG 2203  
QY 572 -----  
Db 2204 ACAAGAACTTCTCCCTAGAGAAATGTCAGAGACATATGGCAAGTACACACAGAT 2263  
QY 572 -----  
Db 2264 GCTGACAGGCTCTGTTATCTGTGACACAGTCTACCAATGCTCCCAACCAATCTCC 2323  
QY 572 -----  
Db 2324 ACCCTGCTAGAGGATGAAGTAATATGCTGTGACAGGATATTCGTTAGAACTGGACCG 2383  
QY 572 -----  
Db 2384 ATAGGCACAGATTAATATCAGCTGAGCAAGTCCAAAGAGAAATGCAAGGTTGGTAGT 2443  
QY 572 -----  
Db 2444 TATGTGGAATGTCACCAAGTGTCTACTCCACAGAGATGTTAGTGTGGCTTGGCCACA 2503  
QY 573 -----LeuValValPhePheSer  
Db 2504 GAAGGAGGAGATGACTTGATGTTATATCCAGAGCTTCAGGAGCTTTGGTGTGTTCTCAGC 2563  
QY 579 LeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerLeuGluTyr 598  
Db 2564 CTCGAGTGACTAAACATGATGTTTTCAGAGATCTGTTTATATAAACTCTCTGGAGTAT 2623  
QY 599 ArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThr 618  
Db 2624 AAAGCCCTGGAGCAAGATCTTAGAATGCTGTGTTCCCTATCTCCAGTCAAACTCAGC 2683  
QY 619 GlyPheLysGluLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLys 638  
Db 2684 GGGTTCAGAACTTAGAAATCTCACTTCAAGATGGCAGATTTGGTGTGATCATCTCGAA 2743  
QY 639 MetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGlu 658  
Db 2744 ATGAAGTTTGGCAATCTGCTCCCTCTCAAGTCAACAATGGGTGTATCATCTCGAA 2803  
QY 659 AspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsn 678  
Db 2804 GACTTTGTACCACTGCCTTACAAATCCATGAACTTGGCTATGATAAATCTCTCTGAT 2863  
QY 679 IleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGln 698  
Db 2864 GTGGATCAGGTGATGAGCCCAACCTTCCAAATTTCCAGGCTGTGAATGATTTTCAGAA 2923  
QY 699 -CysValLysAsn-GluArgThrGluGluAlaGluCysArg 711  
Db 2924 GTGTCTGTGTCACCCCTGGAGTGGAGAAACAAAGTGCAGA 2964

RESULT 11

US-10-007-270-23

; Sequence 23, Application US/10007270

; Publication No. US20020160954A1

## GENERAL INFORMATION:

; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; TITLE OF INVENTION: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 4204  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse IPM 200 cDNA sequence (partial)  
; NAME/KEY: misc feature  
; LOCATION: (1)-(4204)  
; OTHER INFORMATION: n is a, c, g, or t.  
US-10-007-270-23

## Alignment Scores:

Pred. No.:	2,59e-78	Length:	4204
Score:	841.00	Matches:	261
Percent Similarity:	41.20%	Conservative:	123
Best Local Similarity:	28.00%	Mismatches:	238
Query Match:	20.43%	Indels:	310
DB:	13	Gaps:	34

US-10-007-270-2 (1-797) x US-10-007-270-23 (1-4204)

QY 96 TyrTyrArgLeuArgValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAsp 115  
Db 21 TATTTAAAGCCCGAGTGTGGAGAGCCATCTGGAGAGCCCTTCAGGACGTTTGGAT 80  
QY 116 ArgIleProAspThrGluTyrGlnAspTyrPvalSerIleCysGlnGlnGluThrPhe 135  
Db 81 CGACTTCTGGGGTGCATGAATATCGTCACTGATGAATTTATGAGGATGGAGTCACA 140  
QY 136 CysLeuPheAspIleCysLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGln 155  
Db 141 AGTGATTTGAAATGGGCCCTTTAGTCACTGTGGAACATAGAAACCTATATCATG 200  
QY 156 GlnArgIle-----LysGlnArgSerPheProAspArgLysAspGluIleSerAla 172  
Db 201 AAGAACTGGCTTACACAGGAGGAGCTGAGAGAGCTCTCGAAGATCAG---TCCTGT 257  
QY 173 GluLysThrLeuGluPro-----GlyGluThrIleValIleSerThrAspVal 189  
Db 258 GGGCCTGAGTTGTCTTTCAGTTCCTATTGTTGAGACC-----TCAACACTGACA 308  
QY 190 AlaAsnValSerLeuGlyProPhePro-----LeuThrPro 201  
Db 309 GGTGCTGTCTCCAGTCTCTCTATCCAGGGTGGTTCGGAGAGAGCGCAGCGTCACCG 368  
QY 202 AspAspThrLeuLeuAsnGluLeuAspAsnThrLeuAsnAspThrLysMetProThr 221  
Db 369 CAGGAGATATCAGCAATGAAATTT---GAGAAATGTGACAGAGAGGCCCAACACGCT 425  
QY 222 ThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSer 241  
Db 426 GCTGAACAGATTGCGGAATTC-----AGATCCAA 455  
QY 242 LeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGlu 261  
Db 456 CTCTCGGGAAGCGATACAGTGAAGAACTCGGGATCCCTCCAGCGCCCTCTACCGGCTC 515  
QY 262 LeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLys 281



QY 737 CysGluValLeuGlnGlyLysGlyAlaProCysArg 748  
 Db 2688 TGTGACATTATGCTGCGGATGAGGACCATTTGTAGA 2723

## RESULT 12

US-10-198-846-12589  
 ; Sequence 12589, Application US/10198846  
 ; Publication No. US2003009974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Steinmann, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-049  
 ; CURRENT APPLICATION NUMBER: US/10/198,846  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/306,220  
 ; PRIOR FILING DATE: 2001-07-18  
 ; NUMBER OF SEQ ID NOS: 14084  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12589  
 ; LENGTH: 2026  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 1, 2026  
 ; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-12589  
 Alignment Scores:  
 Pred. No.: 4,558-10 Length: 2026  
 Score: 194.50 Matches: 85  
 Percent Similarity: 40.34% Conservativeness: 59  
 Best Local Similarity: 23.81% Mismatches: 146  
 Query Match: 4.72% Indels: 67  
 DB: 14 Gaps: 15

US-10-007-270-2 (1-797) x US-10-198-846-12589 (1-2026)

QY 367 GlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAla 386  
 Db 285 CAGGACAGGAGTGTCACTGTGCCCCCGCCAGCAACAGGAGTTCAGGTTCAGTGCACCC 344  
 QY 387 PheGlyProAspThrGlnSerGluLeuProThrSerPheAlaValIle----- 402  
 Db 345 TGGGACAGGAGTGTCACTCG---GTCCAGTCAACAGGCGGCGGCTGCCACCA 401  
 QY 403 -----ThrGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416  
 Db 402 CGCCAGCCAGAGTGTCACTCAGCCCGGACAAAGCCAGCCCGGCTCCACCGCC 461  
 QY 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr----- 432  
 Db 462 CCCCCAGCCAGCGTGTCACTTCGCGC-----CCGACACAGCAGCGCCCGCC 509  
 QY 433 ---SerTyrSerProAlaMetAlaSerThrSerLeuSerGluAla-----ProPro 449  
 Db 510 GGCTCACCGCCCGCCAGCCCGGTCAGCTGTCACCGCCCGGACACAGCGCCCGCC 569  
 QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 Db 570 GGCTCACCGCCCGCCAGCCCGGTCAGCTGTCACCGCCCGGACACAGCGCCCGCC 605  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSer-----AspTyr 486  
 Db 606 GCCCGGACACAGCGCGCCCGGCTCCACCGCCCGGCTCCAGTGTGTCACCTCG 665  
 QY 487 SerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSer 503

Db 666 GCCCGGACACAGCGCCCGCTTGGCTCCACCGCCCTCCAGTCCCAATGTTCACCTCG 725  
 QY 504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAsp 523  
 Db 726 GCCTCAGGCTCTGCATCAGGCTCAGCTTCTACTCTGTGTGCACACGCGACCTCTCC 785  
 QY 524 LeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSerValPro 543  
 Db 786 GGTACCAACACCCAGCGCAGCAGCAGCTCCA-----TTCTCAATTGCC 830  
 QY 544 AspHisPheLeuGluAspThrThrProVal----- 553  
 Db 831 AGCCACCACTCTGATCTCTATCCACCTTGTGCCAGCATAGCACCAAGAGTGCACGT 890  
 QY 554 -----SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLys 569  
 Db 891 AGCACTCACCATAGCAGGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 950  
 QY 570 GlyArgGluLeuValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSer 587  
 Db 951 TTGTCTACTGGGTCTCTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1010  
 QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
 Db 1011 TCCTCTCTGGAAGATCCCGACGACCTACTACCAAGAGCTGCAGAGAGACATTTCTGAA 1070  
 QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627  
 Db 1071 ATGTTTTTCAGATTATAACAAGGG-----GTTTTCTGGGCTCTCCATATTAA 1124  
 QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
 Db 1125 TTCAGGCCAGGATCTGT 1175  
 QY 648 AsnLeuThrLysAlaValHisGlyVal-----LeuGluAspPheArgSerAlaAla 664  
 Db 1176 -----ACCATCAATGTCACGAGTGGAGACACAGTTCATCATATAAACGGA 1229  
 QY 665 AlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681  
 Db 1230 GCCTCTCGATATAACCTGACGATCTCAGACGTCAGCGTGCAGTGTGTGTGTGTG 1280

## RESULT 13

US-09-964-824A-105  
 ; Sequence 105, Application US/09964824A  
 ; Patent No. US20020102531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horrigan, Stephen  
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
 ; FILE REFERENCE: 689290-73  
 ; CURRENT APPLICATION NUMBER: US/09/964,824A  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/236,033  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US/60/236,032  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US/60/236,028  
 ; PRIOR FILING DATE: 2000-09-28  
 ; NUMBER OF SEQ ID NOS: 583  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 105  
 ; LENGTH: 4139  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-964-824A-105  
 Alignment Scores:  
 Pred. No.: 4,86e-09 Length: 4139  
 Score: 189.50 Matches: 91  
 Percent Similarity: 40.79% Conservativeness: 53  
 Best Local Similarity: 25.78% Mismatches: 132

Query Match: 4.60% Indels: 77  
DB: 9 Gaps: 18

US-10-007-270-2 (1-797) x US-09-964-824A-105 (1-4139)

Qy 385 ProAlaPheGly-----ProAspThrGlnSerGluLeuProThrSerPheAla 400  
Db 2513 CCAGCCACGGTGTACCTCGGCCCGGACACAGG---CCGGCCCGGCTCCACGCC 2569

Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuPro-----ValGlu 416  
Db 2570 CCCCAGCCACCGGTGTACCTCGGCCCGGACACAGG---CCGGCCCGGCTCCACGCC 2629

Qy 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr-----432  
Db 2630 CCCCAGCCACCGGTGTACCTCGGCC---CCGGACACCGCCCGGCCCGC 2677

Qy 433 ---SerTrpSerProProAlaMetAlaSerThrSerLeu-----444  
Db 2678 GGCTCCACCGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2737

Qy 445 ---SerGluAlaProProPheMetAlaSerSerIlePheSerLeuThrAsp-----461  
Db 2738 GGCTCCACCGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2788

Qy 462 ---GlnGlyThrThrAsp-----ThrMetAlaThrAspGlnThr 473  
Db 2789 CCGGCCCGGCTCCACCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2845

Qy 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490  
Db 2846 AGGCCCGGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2905

Qy 491 GlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSerAspSerArg 507  
Db 2906 AGGCCCGGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2965

Qy 508 SerSerAlaGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
Db 2966 GCATCAGGCTCAGCTTCTACTCTGTGTGTCACACAGGACCTCTCGAGGGGTACCAAC 3025

Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 3026 CCAGCCACGAGACATCCCA-----TTCTCAATCCACGACCTCTCTACTGGG 3070

Qy 548 GluAspThrThrProVal-----553  
Db 3071 GATACCTCTACCCCTTCCAGCATAGCACCAAGAGTGTATGCTACCTACCAT 3130

Qy 554 SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeu 573  
Db 3131 AGCTCGTACCTCTCTCCTCCTCCATCCATCAGACACTTCTCCCGAGTTGTCTACTGGG 3190

Qy 574 ValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
Db 3191 GTCTCTTCTTCTCTCTCTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3250

Qy 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValPro 611  
Db 3251 GATCCAGCACCGCACTACTACCAAGAGCTGCAGAGACATTTCTGAAATGTTTTTGCAG 3310

Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGly 631  
Db 3311 ATTATATAACAGGG-----GGTTTCTGGGCTCTCCAAATTAATTAATTAATTAATTA 3364

Qy 632 SerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLys 651  
Db 3365 TCTGTGGTGTACAAATGACTCTGGCCTTCCGAGAGGT-----ACCATC 3409

Qy 652 AlaValHisGlyVal-----LeuGluAspPheArgSerAlaAlaGlnGlnLeu 668  
Db 3410 AATGTCACGACGCTGGAGACACAGTTCATAGTATAAAACGAGACGCTCTCGATAT 3469

Qy 669 HisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681  
Db 3470 AACCTGACATCTCAGACGTCAGCGTGTGATGTGCCA 3508

## RESULT 14

US-09-964-824A-578  
; Sequence 578: Application US/09964824A  
; Patent No. US20020102531A1  
; GENERAL INFORMATION:  
; APPLICANT: Horrigan, Stephen  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-73  
; CURRENT APPLICATION NUMBER: US/09/964,824A  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/60/236,033  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,032  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,028  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 583  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 578  
; LENGTH: 4139  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-824A-578

Alignment Scores:  
Pred. No.: 4,86e-09 Length: 4139  
Score: 189.50 Matches: 91  
Percent Similarity: 40.79% Conservative: 53  
Best Local Similarity: 25.78% Mismatches: 132  
Query Match: 4.60% Indels: 77  
DB: 9 Gaps: 18

US-10-007-270-2 (1-797) x US-09-964-824A-578 (1-4139)

Qy 385 ProAlaPheGly-----ProAspThrGlnSerGluLeuProThrSerPheAla 400  
Db 2513 CCAGCCACGGTGTACCTCGGCCCGGACACAGG---CCGGCCCGGCTCCACGCC 2569

Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuPro-----ValGlu 416  
Db 2570 CCCCAGCCACCGGTGTACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2629

Qy 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr-----432  
Db 2630 CCCCAGCCACCGGTGTACCTCGGCC---CCGGACACCGCCCGGCCCGC 2677

Qy 433 ---SerTrpSerProProAlaMetAlaSerThrSerLeu-----444  
Db 2678 GGCTCCACCGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2737

Qy 445 ---SerGluAlaProProPheMetAlaSerSerIlePheSerLeuThrAsp-----461  
Db 2738 GGCTCCACCGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2788

Qy 462 ---GlnGlyThrThrAsp-----ThrMetAlaThrAspGlnThr 473  
Db 2789 CCGGCCCGGCTCCACCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2845

Qy 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490  
Db 2846 AGGCCCGGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2905

Qy 491 GlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSerAspSerArg 507  
Db 2906 AGGCCCGGCCCGGCTCCACCTCGGCCCGGACACAGG---CCGGACACCGCCCGGCCCGC 2965

Qy 508 SerSerAlaGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
Db 2966 GCATCAGGCTCAGCTTCTACTCTGTGTGTCACACAGGACCTCTCGAGGGGTACCAAC 3025

Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 3026 CCAGCCACGAGACATCCCA-----TTCTCAATCCACGACCTCTCTACTGGG 3070

Qy 548 GluAspThrThrProVal-----553  
Db 3071 GATACCTCTACCCCTTCCAGCATAGCACCAAGAGTGTATGCTACCTACCAT 3130

Qy 554 SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeu 573  
Db 3131 AGCTCGTACCTCTCTCCTCCTCCATCCATCAGACACTTCTCCCGAGTTGTCTACTGGG 3190

Qy 574 ValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
Db 3191 GTCTCTTCTTCTCTCTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3250

Qy 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValPro 611  
Db 3251 GATCCAGCACCGCACTACTACCAAGAGCTGCAGAGACATTTCTGAAATGTTTTTGCAG 3310

Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGly 631  
Db 3311 ATTATATAACAGGG-----GGTTTCTGGGCTCTCCAAATTAATTAATTAATTAATTA 3364

Qy 632 SerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLys 651  
Db 3365 TCTGTGGTGTACAAATGACTCTGGCCTTCCGAGAGGT-----ACCATC 3409

Qy 652 AlaValHisGlyVal-----LeuGluAspPheArgSerAlaAlaGlnGlnLeu 668  
Db 3410 AATGTCACGACGCTGGAGACACAGTTCATAGTATAAAACGAGACGCTCTCGATAT 3469

Db 2966 GCATCAGCTCAGCTTCTCTCTGGTGCACACCGGACCTCTGCCAGGGGTACCAACACC 3025  
Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 3026 CCAGCCAGCAGAGCACTTCA-----TTCTCAATTCCAGCCACCACTCT 3070  
Qy 548 GluAspThrThrProVal-----553  
Db 3071 GATACCTCTACCACTTCCAGCTGACCAAGCAAGCACTGATGCCAGTACCACTCACCAT 3130  
Qy 554 SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeu 573  
Db 3131 AGCTCGGTACCTCTCTCACCTCTCTCAATCAGCAGCACTTCTCCCAAGTTGTCTACTGGG 3190  
Qy 574 ValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
Db 3191 GTCTCTTTCTTTCTCTCTCTTTTTCACATTTCAAACTCCAGTTTAAATCTCTCTCGAA 3250  
Qy 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuValPro 611  
Db 3251 GATCCAGCAGCAGTACTACCAAGAGCTGCAGAGACATTTCTGAATGTTTTTGCAG 3310  
Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluLeuLeuAsnPheArgAsnGly 631  
Db 3311 ATTTATAAACAAAGG-----GGTTTCTGGGCTCTCTCAATATTAAAGTTTCAGGCCAGGA 3364  
Qy 632 SerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLys 651  
Db 3365 TCTGTGGTGTAACATTGACTCTGGCTTCGAGAAGGT-----ACCATC 3409  
Qy 652 AlaValHisGlyVal-----LeuGluAspPheArgSerAlaAlaGlnGlnLeu 668  
Db 3410 AATGTCCAGCAGTGGAGACACAGTTCATCAGTATAAAACGGAAGCAGCTCTCGATAT 3469  
Qy 669 HisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681  
Db 3470 AACCTGAGATCTCAGACGTCAGCGTGGGTGATGTGCCA 3508

## RESULT 15

US-09-864-864-334  
; Sequence 334, Application US/09864864  
; Patent No. US20020102679A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Secretist, Heather  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steve P.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Carter, Derrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.523  
; CURRENT APPLICATION NUMBER: US/09/864,864  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: Corixa Invention Disclosure Database  
; SEQ ID NO 334  
; LENGTH: 4139  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-864-864-334

## Alignment Scores:

Pred. No.:	4,86e-09	Length:	4139
Score:	189.50	Matches:	91
Percent Similarity:	40.79%	Conservative:	53
Best Local Similarity:	25.78%	Mismatches:	132
Query Match:	4.60%	Indels:	77

DB: 9 Gaps: 18  
US-10-007-270-2 (1-797) x US-09-864-864-334 (1-4139)  
Qy 385 ProAlaPheGly-----ProAspThrGlnSerGluLeuProThrSerPheAla 400  
Db 2513 CCAGCCAGCAGGTGTACCTCGGCCCGGACACACAGG---CCGGCCCCGGGTCCACCGCC 2569  
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416  
Db 2570 CCCCCAGCCACGGGTGTACCTCGGCCCGGACACACAGGCGCGGGGTCCACCGCC 2629  
Qy 417 ProGlnLeuGluThrValAspGlyValGluHisGlyLeuProAspThr-----432  
Db 2630 CCCCCAGCCACGGGTGTACCTCGGCC-----CCGGACACAGCGCGGCCCGC 2677  
Qy 433 ---SerTyrSerProProAlaMetAlaSerThrSerLeu-----444  
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Qy 462 ---GlnGlyThrThrAsp-----ThrMetAlaThrAspGlnThr 473  
Db 2789 CCGGCCCGCGGTGTACCTCGGCCCGCCAGCCCGGTGTACCTCGGCCCGGAC---ACC 2845  
Qy 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490  
Db 2846 AGCGCGGCCCGGGTGTACCTCGGCCCGCCAGCCCGGTGTACCTCGGCCCGGACAAAC 2905  
Qy 491 GlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSerAspSerArg 507  
Db 2906 AGGCGCGCTTGGGTGTACCTCGGCCCGCCAGTCCACATGTCACTCGCGCTCAGGCTCT 2965  
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Db 2966 GCATCAGCTCAGCTTCTACTCTGGTGCACAAACCGCACCTCTGCCAGGGTACCAACACC 3025  
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Qy 548 GluAspThrThrProVal-----553  
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Qy 554 SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeu 573  
Db 3131 AGCTCGGTACCTCTCTCACCTCTCTCAATCAGCAGCACTTCTCCCAAGTTGTCTACTGGG 3190  
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Db 3410 AATGTCCAGCAGTGGAGACACAGTTCATCAGTATAAAACGGAAGCAGCTCTCGATAT 3469  
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Db 3470 AACCTGACGATCTCAGACGTCAGCGTGAGTGAGTGATGTCGA 3508  
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Search completed: March 2, 2004, 00:55:48  
Job time : 790 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 20:33:11; Search time 146 Seconds

(without alignments)  
3029.424 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117  
Sequence: 1 MYLETRRAIFVFWIFLQVQ.....NSLLTVYBEFNFHQWEGN 797

Scoring table:

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US10007270/runat\_25022004\_164208\_27225/app\_query.fasta\_1.967  
-DB=Issued Patents NA -QWMT=fastcap -SUFFIX=xni -MINMATCH=0.1 -LOOPGL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	157	3.8	19307	3	US-08-836-022A-10
C 2	157	3.8	19307	3	US-09-427-048A-10
C 3	146	3.5	8982	3	US-08-976-355-5
4	145.5	3.5	6192	2	US-08-479-537A-1
5	145.5	3.5	6192	3	US-09-083-116-1
6	145.5	3.5	6192	4	US-03-134-916A-1
7	145	3.5	8224	6	5180808-1
8	144.5	3.5	3104	4	US-09-418-780A-2
9	144.5	3.5	3106	4	US-09-392-714-4
10	141.5	3.4	6407	2	US-08-616-844-7
11	141.5	3.4	6407	2	US-08-599-854-7
12	141.5	3.4	6407	3	US-08-944-868A-7

13	141.5	3.4	6407	3	US-08-944-423A-7	Sequence 7, Appli
14	141.5	3.4	6407	3	US-08-944-496-7	Sequence 7, Appli
C 15	138	3.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
16	137.5	3.3	2156	1	US-08-178-477B-31	Sequence 31, Appli
17	137.5	3.3	2156	4	US-09-304-121-1	Sequence 11, Appli
18	137.5	3.3	2156	4	US-09-023-655-1111	Sequence 1111, Ap
19	137.5	3.3	2458	4	US-09-513-783A-175	Sequence 175, App
C 20	135.5	3.3	2835	4	US-09-134-001C-1515	Sequence 1515, Ap
C 21	135.5	3.3	3561	4	US-09-134-001C-1685	Sequence 1685, Ap
22	135.5	3.3	4928	4	US-09-620-312D-329	Sequence 329, App
23	135.5	3.3	6414	4	US-09-134-001C-1626	Sequence 1626, Ap
C 24	135.5	3.3	13977	4	US-09-484-970B-60	Sequence 60, Appli
C 25	134.5	3.3	8312	4	US-09-620-312D-1048	Sequence 1048, Ap
26	134	3.3	13473	5	PCT-US96-03916-1	Sequence 1, Appli
27	134	3.3	18912	5	PCT-US96-03916-59	Sequence 59, Appli
28	131.5	3.2	3073	4	US-09-620-312D-279	Sequence 279, App
29	131	3.2	4822	4	US-09-484-970B-106	Sequence 106, App
30	130.5	3.2	5494	3	US-08-910-864-10	Sequence 10, Appli
31	130.5	3.2	5510	1	US-08-123-161A-7	Sequence 7, Appli
32	130.5	3.2	5510	1	US-08-483-278-7	Sequence 7, Appli
33	130.5	3.2	5645	4	US-09-023-655-1319	Sequence 1319, Ap
34	130.5	3.2	5681	4	US-09-919-172-58	Sequence 58, Appli
35	130	3.2	3573	4	US-09-107-532A-3492	Sequence 3492, Ap
C 36	129	3.1	3540	4	US-09-976-594-888	Sequence 888, Appli
C 37	128.5	3.1	1830121	4	US-08-557-884-1	Sequence 1, Appli
C 38	128.5	3.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
39	128	3.1	5952	4	US-09-687-875A-1	Sequence 134, App
40	127.5	3.1	4323	4	US-09-620-312D-134	Sequence 23, Appli
41	127.5	3.1	5933	4	US-09-919-172-23	Sequence 2, Appli
42	127	3.1	9626	4	US-09-150-867-2	Sequence 30, Appli
43	126.5	3.1	14770	4	US-09-220-132-30	Sequence 39, Appli
44	126	3.1	4522	4	US-08-956-171E-39	Sequence 5, Appli
45	126	3.1	8789	1	US-08-328-254-5	

#### ALIGNMENTS

RESULT 1  
US-08-836-022A-10/c  
Sequence 10, Application US/08836022A  
Patent No. 6001557  
GENERAL INFORMATION:  
APPLICANT: Trustees of the University of Pennsylvania  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Chen, Shu-Jen  
APPLICANT: Weitzman, Matthew  
TITLE OF INVENTION: Improved Adenovirus Virus and  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, P O Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836.022A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/331,381  
FILING DATE: 28-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNPVN.008PCT  
TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-540-9200  
 ; TELEFAX: 215-540-5818  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 19307 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 US-08-836-022A-10

## Alignment Scores:

Pred. No.: 0.000161 Length: 19307  
 Score: 157.00 Matches: 173  
 Percent Similarity: 35.60% Conservative: 151  
 Best Local Similarity: 19.01% Mismatches: 318  
 Query Match: 3.81% Indels: 268  
 DB: 3 Gaps: 44

US-10-007-270-2 (1-797) x US-08-836-022A-10 (1-19307)

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 QY 33 ThrLysAspIleAspAsnProArgAsnGluThrThrGluSerThrGluLysMetTyr 52  
 DB 8308 CGGATTGATATTATTCACAAGNAGNAGACAGCGCTTGCAAGTGCACCTCCATGGAA 8249  
 QY 53 LysMetSerThr-----MetArgArg 59  
 DB 8248 AAGGTGAAGTACAGGAAGCGGTGGCACAGATGGATTTCAGGGGGAAGAACTTCATAGA 8189  
 QY 60 llePheAspLeuAlaLysHisArgThrLysArgSerAla-----PhePhePro 75  
 DB 8188 ATGTACAAGCAAGCAAGGCGGAGATCGACAGATCAGTTGAAAATGGCGACATTTTCAT 8129  
 QY 76 ThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAla 95  
 DB 8128 TATGATATGAAGTA-----TTTAATCAATGGCTGAATGAAGTTGAACAG 8084  
 QY 96 TyrTyrArgLeuArgValCysGlnGluAlaValTrpGlu-----AlaTyrArgIlePhe 113  
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 DB 8026 CTTAAGGAACTCCAGATGGCATTTGGGCGCGTCAGCTGTTGTCAGAACACTGAATGCA 7967  
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 DB 7942 -----TCITCAAAAACAGATGCAATATTCACAGAAAATATTAGGA 7901  
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 QY 171 SerAlaGluLysThrLeu-----GlyGluProGlyGluThrIleValle 185  
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 DB 7405 GGACCGTTTGATATAAGAGATT-----GAAGTAACAGTTCACGGT----- 7364  
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 QY 363 -----LeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
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QY 171 SerAlaGluLysThrLeu-----GlyGluProGlyGluThrIleValIle 185  
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QY 323 LeuSerPheAspSerAsnLysIleGluSerGluValTyrHisGlyThrMetGluGlu 342  
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DB 7327 CAGCATTGTATAGGAAAA----- 7307  
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DB 7306 -----CCAGCACTCAG----- 7295  
QY 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
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QY 421 ThrVal-----AspGlyAlaGluHisGlyLeu----- 429  
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QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564  
DB 6928 -----TTGGAACAGAGACGCCCC-----CAATTGGAAGAACTCATTTACTGCTGCCAG 6881  
QY 565 ThrIleAlaProLys-----GlyArgGlnLeuValValPhePheSerLeuArgValAla 582  
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QY 583 AsnMetAlaPheSer----- 587  
DB 6820 AGAATTCAGATTCAGTGGGTGAGGTTCAAGAACAGCTGCAGAACAGGAGACACAGTTG 6761  
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
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QY 608 LeuLeu----- 611  
DB 6703 GTCATAGGACAGCTCAGAGGCAAGCTTGACTCATGTAAGAAAGAGTCTCTCACAGTAGAT 6644  
QY 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeu---GluIleLeuAsnPheArgAsn 630  
DB 6643 GCAATCCAAAGAAAGATCACAGAAACCAAGCAGTTGGCCAAAGACCTCGTCAACGGCAG 6584  
QY 631 GlySerValIleVal-----AsnSerLysMetLysPheAlaLysSerValProTyrAsn 648  
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QY 649 LeuThrLysAlaValHisGlyValLeuGluAspPhe----- 660  
DB 6523 GATACCGAAAGATACACATGATATACAGAGATATCAATCTTCTTGGGAACATTCAT 6464  
QY 661 -----ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyr 675  
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QY 676 SerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGlu 695  
DB 6403 CCTCTGACCTGGAG-----AAGTTCTTCTCTGGATTACG 6368  
QY 696 PheAlaGlnCysValLysAsn-----Glu 703  
DB 6367 GAAGCAGAAACAACTGCCAATGCTCTACAGGAGCGTTCCTCGTAAGGAGAGCTCTAGAA 6308  
QY 704 ArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAsp 723  
DB 6307 GACTCCAGGGAGTCAGAGAGCTGATGAACCAATCGCAAGATCTCCAGAGAGAAATTGAA 6248  
QY 724 -----GlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740  
DB 6247 ACTCACACAGATATCTATCACAACTTTGATGAAATGGCCAAATAAATCCTGAGATCCCTG 6188  
QY 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760

Db 6187 GAAGGTCGGATGAAGCACCCTCTTACAAAGACGTTTGGATACATGAATTTCAAGTGG 6128  
 QY 761 Ser-----ValLysLysPheGlnAsnGlnGlnAsnAsnLysValLysSerLysArgAsn 778  
 Db 6127 AGTGAACCTTCAGAAAGATCTCTCAACATTAGGTGCCCATTTGGGAAGCAAGTTCTGACCAG 6068  
 QY 779 SerGluLeuLeuThrValGluLysGluGlu 788  
 Db 6067 TGGAGCGTTTGATCTTCTCTTCAGGAA 6038

## RESULT 3

US-08-976-255-5  
 ; Sequence 5, Application US/08976255  
 ; Patent No. 6136581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jono, Keith E.  
 ; APPLICANT: Plowman, Gregory  
 ; TITLE OF INVENTION: KINASE GENES AND USES  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/976.255  
 ; FILING DATE: No. 6136581ember 21, 1997  
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/031,675  
 ; FILING DATE: No. 6136581ember 22, 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 229/182  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 982 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-976-255-5

Alignment Scores:  
 Pred. No.: 0.000616 Length: 8982  
 Score: 146.00 Matches: 175  
 Percent Similarity: 32.72% Conservative: 109  
 Best Local Similarity: 20.16% Mismatches: 302  
 Query Match: 3.55% Indels: 283  
 DB: 3 Gaps: 38

US-10-007-270-2 (1-797) x US-08-976-255-5 (1-8982)

QY 40 ProArgAsnGluThrThrGluSerThrGluLysMetTyrlsMetSerThrMetArgArg 59  
 Db 2203 CCITTCACATATATTATGATGTGGACAAATCGGAGATTGGCCAGTCCACCAAAA 2262  
 QY 60 IlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLys 79  
 Db 2263 ATATTCGACTTAATGGAATTAACGGAGTTCAACGGCGACTTTAAACCTGCCACTTTAAGT 2322

QY 80 ValCys-----ProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyr 96  
 Db 2323 TCCAGTTGGATAAACCCCAAGAGTCAGTC----- 2352  
 QY 97 TyrArgLeuArgValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArg 116  
 Db 2352 ----- 2352  
 QY 117 IleProAspThrGlyGluTyrGlnAspTrpVal-----SerIleCysGlnGlnGluThr 134  
 Db 2353 -----ATAACAGGCCACTTTTGAGAAAGAAAGCCCGCTAAGATTTTTCACAGTCAGCCT 2406  
 QY 135 PheCysLeuPheAsp----- 139  
 Db 2407 CTCCTGCCTATCAGATAATCTTATGACCACCAAGATAATTTTGATTCATTTGAATGTTCAAGAA 2466  
 QY 140 IleGlyLysAsnPhe-----SerAsnSer 147  
 Db 2467 TTGTCAGAAACTTTTATTCTTCAAGAGAAACTTACTTAAAGGGCTCATTTGTCACG 2526  
 QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 Db 2527 AAAGAACACATAAATGATCTTCAGACAGAACTTAAGATGCTGTTTACTGAGAGCTATG 2586  
 QY 168 AspGluIleSerAlaGluLysThrLeu-----GlyGluPro 179  
 Db 2587 TTAGAAACGTCTAGTAAACTCTTTAGACTAGCTTTCAGTTTGTGTAATAAGCA 2646  
 QY 180 GlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeu 199  
 Db 2647 GGC-----TTGTCTTGTTCAGGAAACCTAAGC-----ACA 2679  
 QY 200 ThrProAspAspThr-----LeuLeuAsnGluIleLeuAspAsnThrLeuAsn--- 215  
 Db 2680 AAGGTGACGATACAGATGCTGCTACAGTGACACTTTGACCACTCATTTGAGTCT 2739  
 QY 216 -----AspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGlu 233  
 Db 2740 TCCCGGAAGTGCAGGTACCTCTACCTCTCTGAAACAGAGAAACCCCGCTGGGTA 2799  
 QY 234 GlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAsp 253  
 Db 2800 CCCCAGACTCACTCCCAACACAGGAGAAACCCAGCCCGCTGTTAGATGTTATTGTC 2859  
 QY 254 SerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIle 273  
 Db 2860 CCGGAGGACTCTCCACCAGACATCAGTCCACAGCTGTGACTGTCCCGGTGAAAT 2919  
 QY 274 PheLysLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLysLysGlu 293  
 Db 2920 -----CTCTCAACTGATGCCAGAACCCACAGCCTGGATAACAGG---TCCACAGAC 2967  
 QY 294 LysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAla 313  
 Db 2968 TCTCTGCGAGATGAGGAGACCTCGGACTACC-----GAAAGTACTCTGTT 3018  
 QY 314 GluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGlu---Ser 332  
 Db 3019 CTTGCTGATGATCATCTTCCAGCAGCGGTGAGTGTAGGAGTAGTCTCCCGGAACCTGGA 3078  
 QY 333 GluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAla 352  
 Db 3079 CAGGAATTCACATAAACCAATTTTCGGAAGACCATCAGCTCAT----- 3123  
 QY 353 ThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGly 372  
 Db 3124 -----CCCGGCTAGAGAAAAACTTAGAGCTGTGGAGACTTTAAATCAGCTC 3171  
 QY 373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392  
 Db 3172 AATTCTAAGACGACCAAGAAAGACAGGCTTGTGCTCTCCTCTCCTCGGACTCA--- 3228

393	QY	SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu	412
3229	Db	 -----ACACGTACGACGAGCTCTCTGGAGGAC-----AGTTGTTCAGCACCCCTTC	3273
413	QY	ProProValGluProGlnLeuGluThrValAspGlyAlaGlu-----	426
3274	Db	CCAGCCTCTGAGCGCTCCCTGGAAACCCCGAGATCTCTCGAGTCAGTGATGTCACGAA	3333
426	QY	-----	426
3334	Db	GGCTACTGGAGCTCTTTAGGATCTCACACTCCCGAGAAACTAGTGCCTCCCGATAAGCG	3393
427	QY	-----HisGlyLeuProAspThrSerTyrSer---ProProAla	438
3394	Db	GCAGACAGTGCTGTACGAAAACAGAGAACTTGGAGTCTCCGAGTGGACCTTCATCCCGCT	3453
439	QY	MetAlaSerThrSerLeuSerGlu-AlaProProPhePheMetAlaSerSerIlePheSe	458
3454	Db	CCCGAGGACACCGCAGACTCAGAACAGCCACCACGGCGATGGCGGCACAGCGGTCTG	3513
458	QY	rIeuThrAspGlnGlyThr-----	464
3514	Db	CTTCCCAACCCGGTCAATTGTCATCTCAGATGCCGCGCATGGTTCACAGAGGCACAGAA	3573
465	QY	-----ThrAspThrMetAlaThrAspGl	472
3574	Db	ACCCCTGAGACGTTTCACAGCTGGCTCCAGGGTTTCATCCGAGACTCTCGGTACTTCTCA	3633
472	QY	nThrMet---LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGl	491
3634	Db	GACATGACTCTGAGCCCGAGAAAAGGTCTGAGAGGTCCCGGA-ACCTCCCATCCGC	3692
491	QY	nLeuAlaLeuGlyIleSerHisPro-----ProAl	501
3693	Db	CTTGGTGTGTACAGAGCAGGCCCTTACCAGGACGAGTCCTCCCGAGCAAGTCTCTGC	3752
501	QY	sSerSerAsp-----AspSerArgSerSerAlaGlyGlyGluAspMetVala-rHi	518
3753	Db	TGCCCAGGATAGTGCCTCGGAAGCCAGAAAGACCCAGCCAGATGAAAGTTCTGTCTGTC	3812
518	QY	sLeu-----AspGluMetAspLeuSerAspThrProAlaProSerGlu-----Va	533
3813	Db	TTTGCACTCCAGTGAAGTTAGAGCCAGCCGCGAGCCAGCACAGACTGTGTGT	3872
533	QY	lProGlu-----LeuSerGl	538
3873	Db	TCCCGACAGGTGCATCCACGGAAGCAGAGGCCAGCAGTCCCTGAGTGTGCTGAATGC	3932
538	QY	uTyrValSerValProAspHisPhe---LeuGluAspThrThrProValSer-----	554
3933	Db	AGAACTTAGCGCGCGATGACTTCGAGACACAGGACGATCCGCCCTGCACCTCGCTTC	3992
555	QY	-----AlaLeuGlnTyrIleThrThr---	561
3993	Db	CACGGGACCAACACGAACTCCTTGCCTACACCAATTCTGCGCTGGCAAGTCCCT	4052
562	QY	-SerSerMetThrIleAlaProTyrGlyArgGluLeuValval-----PhePh	577
4053	Db	GTCCAGCCACTCCGAGGCGGCCGAAGTTGAGGACCGGCACATCGAAGGAAGTACCTGGG	4112
577	QY	eSerLeuArgValAlaAsnMetAla---PheSerAsnAsp-----	589
4113	Db	GAACCTCGGGGTGTCCGGGATGCTCGACCTCTCAGAGGACGGGATGGATGACAGCAGGA	4172
590	QY	-----LeuPheAsnLysSerSerLeuGl	597
4173	Db	GGACGAAACACGACGACTCGACGAGGACCTTGCGGGCTTCAACTCTGCATAGCTCAG	4232
597	QY	uTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLe	617
4233	Db	CTCCGAGTCGGAGGACGAG-----ACCGAGCACCCCGTGCCCATCATCTCTCAGCAACGA	4286
617	QY	uThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSe	637

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Db      4287  GGACGGAAGCACCTGCGGAGTCTGTGTGAAG----- 4317
QY      637  rLYsMetLYsPheAlaLYsSerValProTYrAsnLeuThrLYsAlaValHisGlyValle 657
Db      4318  -----CCACAGCGGCCAATGCCCCCGACCACTGCC----- 4350
QY      657  uGluAspPhe---ArgSerAlaAlaLaGlnGlnLeuHisLeuGluLeuAspSerTYrse 676
Db      4351  -GAGGACTCGAAGAAAGAAAGAGGCATCGTCTTTTCGATGATGTCCAGTCTACCT 4409
QY      676  rLeuAenIlleGlu---ProAlaAspGlnAlaAspProCysLYsPheLeuAlaCysGlyG1 695
Db      4410  GTTTCACGAGGAGACCCCAACCAAGAGCTGGGGCCCTGTGGAGGAGAGCGTGGCGCCC 4469
QY      695  u-----PheAlaGlnCysValLYsAs 702
Db      4470  GGACCTGAGCGGCCAGCCCCAGCCTCAGGCTTCCTCCTACCTGAGCAGTGCATCAATC 4529
QY      702  nGluArgThrGluGluAlaGlu 709
Db      4530  CGAAGCTCCACCGACGAAGA 4551

RESULT 4
US-08-479-537A-1
; Sequence 1, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBERN, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs

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5245	TCCACGGCCCTCCAGCTCCACAAATGCTCACCTCGGCTCAGGCTCTGCATCAGGCTCAGCT	5304
513	GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGlu	532
5305	TCTACTCTGTGTGACAAACGGCACCTCTGCCAGGGTACCACAAACCCAGCCAGCAAGAGC	5364
533	ValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThrPro	552
5365	ACTCCACCC-----AGCATTCACGCCACCACTCTGTATACTCTCTACCAACC	5409
553	Val-----SerAlaLeuGlnTyr	558
5410	CTTCGCCACCATAGCACCAAGACTGATGCCAGTAGCACTCCACATAGCACGGTACTCTCT	5469
559	IleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePhe---	577
5470	CTCACCTCTCTCAATCACAGCACTCTCTCCAGTTGTCCTACTGGGTCTCTTCTTTTC	5529
578	---SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeu	596
5530	CTGTCTTTTCATTTCAAACCTCCAGTTTAACTCTCTCTGGAAGATCCAGCACCGAC	5589
597	GluTyrArgAlaLeuGluGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsn	616
5590	TACTACCAAGAGCTGCAGAGACACTTCTGAAATGTTTTGCAGAAATTATAACAAGGG	5649
617	LeuThrGlyPheLysGlnLeuGluLeuAsnPheArgAsnGlySerValIleValAsn	636
5650	-----GTTTTCTGGGCTCTCCAATTAAGTTTCAGGCCAGAAATCTGTGGTGTACAA	5703
637	SerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyVal	656
5704	TTGACTCTGGCTTCCGAGAGGT-----ACCATCAATGTCACGACGTG	5748
657	-----LeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAsp	673
5749	GAGACACAGTTTCAATCAGTATAAAACGGAAGCAGCTCTCGATATAACGTACGATCTCA	5808
674	SerTyrSerLeuAsnIleGluPro	681
5809	CAGCTCAGGTGAGTCATGTGCCA	5832

RESULT 5

US-09-083-116-1

; Sequence 1, Application US/09083116

; Patent No. 6203795

GENERAL INFORMATION:

APPLICANT: CHAMRON, Pierre

APPLICANT: KIENY, Marie-Paule

APPLICANT: LATHE, Richard

APPLICANT: HAREUVENI, Mara

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE

TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/083,116

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/479,537

FILING DATE:









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QY 479 LeuThrIleProThrSer----- 484
Db 5859 ATAGACGTCGGCTCATCTGTAATGTGCCACAGGATTTCTTTAAGGAAATTCATGTAAAT 5918
QY 485 -----AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProAla 501
Db 5919 ATTGAAGCAACTTTCAAACCATCAAGTGAAGAAATACCTTCACATACCTGACCCCTCCCTCT 5978
QY 502 SerSerAspSerArgSerSerAlaGlyGlyLeuAsp---MetValArgHisLeuAsp 520
Db 5979 TTATCTCTCTGACACAAATATAGAACCTTCAGAAAGATGATGTAACCTGAGTTATTAGAA 6038
QY 521 GluMetAspLeuSerAspThrProAla----- 529
Db 6039 GAATGGAGAGCTTCTCCACAGAACTTATCTGCTGGAGGAAGTGAATCTCCAAGAT 6098
QY 530 -----ProSer--- 531
Db 6099 TTCAAAACAAAACCGATGTTCAAGTTCTCGAGAAGCAATCAAGATGTTCCACACCAT 6158
QY 532 GluValProGluLeuSerGluTyrValSerValProAspHisPhe---LeuGluAspThr 550
Db 6159 AAACACCTGAGGCTGGAACCTGTTATTACAACTGCCGATGAAATGAATTAGAGGTGCT 6218
QY 551 Thr----- 551
Db 6219 ACACAGTGGCCACACTCTACTCTCTCTCCACCTATGGGTCGAGGAGGTGGTG 6278
QY 552 -----ProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
Db 6279 CTTGGCTPAAGTCCACAGACTTTCGAGAGGCCACGCTTCTCTCTCCAGAAATAAAC 6338
QY 568 Pro-----LysGlyArgGluLeuValPhePheSerLeuArg 580
Db 6339 CCTGAACTCAAGCAGCTTTAATCAGAGGCGGAGATTCACGATAGCAGCATCAGAACAC 6398
QY 581 -----ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyr 598
Db 6399 CAAGTGGCAGCGAGAAATCTTGATTCATGATCAGGCAACAGTAACCTGTGGAAATTT 6458
QY 599 ArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThr 618
Db 6459 AAT-----ACTGAGGTGCAACACCAACCATTTTCCCTTCCTGGAGACT 6500
QY 619 Gly-PhelysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAlaAsnSerLy 638
Db 6501 TCTAATGAACAGATTTCTCTGATTG-----GCATTAATGAAGAGTCA 6542
QY 638 sMetLysPheAlaLysSerValProTyrAsnLeu-----ThrLysAlaVal 653
Db 6543 GTGGAAGGCACGCGCAATCTATTACAGGACCTGATCGCTGCAAAATGMAACCGTGCCTT 6602
QY 653 lHisGlyValLeuGluAspPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluLeAs 673
Db 6603 A-----ACGAGGCGACCTGTTACTCTGAACTTCC 6635
QY 673 pSerTyrSerLeuAsnIleGlu-----ProAlaAspGlnAla-----AspPr 687
Db 6636 TACGTATGCACC-TGTGTGCCAGGATACAGCGGAGACCACTGTGAACTTGATTTGATGA 6694
QY 687 oCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGl 707
Db 6695 ATGTCACCTTAATCCCTGTCGTAAATGAGGACCACTGTGTTGATGGTTTAAACACA----- 6749
QY 707 uAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPr 727
Db 6750 -TTCAGGTGCTCTGCCTTCCAGTTATGTGT----- 6782
QY 727 oGlyLeuCysGlyProGlyThrLysGluCysGluVal-----LeuGlnGlyLy 743
Db 6783 -GCACITTTGTGACAGATACCGAGACATGTGACTATGCTGGTGCCACAAATTCAGAGGCA 6841
QY 743 s-----GlyAlaProCysArgLeuProAspHisSerGluAsnGln----- 756
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Db 6842 GTGCTACAAATACTTTTGGCCCATCGACGCGCATGGGATCGAGCTGAACGGGAATCGCGTCT 6901
QY 757 -----AlaTyrLysThrSerValLysLysPheGlnAsnGlnGln----- 769
Db 6902 GCAGGTGCGCCATCTTCAAGCATCTCTGCTCCAGGAACAAATGTTTGTAAATCGTGT 6961
QY 770 -----AsnAsnLysValIleSerLys-----ArgAs 778
Db 6962 GGCCCATGATTATCAGTGGATAGGCTCAATGACAAGATGTTTGAGCATGACTTCGGTTG 7021
QY 778 nSerGluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797
Db 7022 GACTGATGCGACACACTGCAATACGAG-----AATTGGAGACCCCAAC 7064

RESULT 8
US-09-418-780A-2
; Sequence 2, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/J998/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(2946)
US-09-418-780A-2

Alignment Scores:
Pred. No.: 0.000136 Length: 3104
Score: 144.50 Matches: 150
Percent Similarity: 34.23% Conservative: 116
Best Local Similarity: 19.31% Mismatches: 321
Query Match: 3.51% Indels: 191
DB: 4 Gaps: 32

US-10-007-270-2 (1-797) x US-09-418-780A-2 (1-3104)
QY 16 LeuGlnValGlnGlyThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAsp 35
Db 764 CTGCAACTTCAGCAGTTAAAGCAAGTAGTAGTAATTTCTCCAAACATTCACAGAA-AAATCA 822
QY 36 Ile-----AspAsnProProArgAsn----- 42
Db 823 GTGGCAGCTGCCACCTATAAAAGAAAATATGCAAAAGATGTTTCCAGATTCACAGAA 882
QY 43 -----GluThrThrGluSerThrGluLysMetTyrLysMetSerThrMet 57
Db 883 CAATATAATGTTGGAGACTGTTAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 942
QY 58 ArgArgIlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePhe---ProThr 76
Db 943 CTTAAAGAAATGCTTCAAGAAACATTTTTCATGATGCGCCCTTTTATATCCTGTT 1002
QY 77 GlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyr 96
Db 1003 GACCTTAATGCTTTG-----GGACTCCATAACTACTATGACGTTGTCAAAATCCG 1053
QY 97 TyrArgLeuArgValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArg 116
Db 1054 ATGATCTTGAACACTATTAGGAGAAATG----- 1093
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117 IleProAspThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnLeuThrPheCys 136  
1084 -----GATAACCAAGAAATATAAGGATGCATCTCAATTTGGGCA----- 1122  
137 LeuPheAspIleGlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGln 156  
1123 -----GATGTAGATTATGTTCTGATGCTCAAGTAC----- 1158  
157 ArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeu 176  
1159 -----AATCCTCCAGATCAGCAAGTTGACAAATGGCAAGAATGCTT 1200  
177 GlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyPro 196  
1201 CAGGAT-----GTTTCCGAACGCAATTTTCAAGATCCCGAATGAACCT 1245  
197 PheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAsp 216  
1246 GTTGAGAGATGCTTTATGTTTACATCAAAACAGATATACAGAAACCCACTGGTAGAG 1305  
217 ThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArgVal 236  
1306 AACACTAATGAAGCTCTCTGAGGGAACCTCTCTGATGATTTCTGAGATGAGCGAGTT 1365  
237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256  
1366 -----AAGCGTCTTGCAAGCTTCAGGAGCAGCTTAAA 1398  
257 ProTyrTyrGlnGluAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLys 276  
1399 GCTGTACATCAACAGCTCCAGCTTTGTCCCAAGTACCTTTCCCTAAGCTAAATAAAG 1458  
277 LeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGly 296  
1459 AAAGAGAGCTTAAAG-----GAAAGAAAAAGAAAGGTTAAT 1500  
297 SerSerSer-----ThrGluMetGlnLeuThrAlaIlePheLys 309  
1501 AACAGCAATGAAATCCCAAGAAAAATGTGTGAGCAATGAGGCTAAAGGAAAGTCCAA 1560  
310 ArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLys 329  
1561 AGAAAT-----CAGCCAAAGAAAGAAAGAAACAACAGTTTCATTGT----- 1599  
330 IleGluSerGluGluValIleHisGlyThrMetGluGluAspLysGlnProGluIleTyr 349  
1600 CTAAATCTGAAGAT-----GAGATAATGCTAAACCTATGAACAT 1641  
350 LeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeuGluGluGlnSerLeu 369  
1642 -----GATGAGAAAGGAGGTTAAGTCTGATATATAACAAACCTCCCTGGAGAT 1689  
370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
1690 AAACCTGGCGAGTA-----GTTACATATATACATCAAGAGAGCCTTCTCTGAGCAAT 1743  
390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
1744 TCCAAATCTGTGATGATAGATAGACTTTGAAACACTGT-----AAGCATCAACACTAAGA 1800  
410 ProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeu 429  
1801 -----GAATTAGAAAAATATGTTTCGGCA-----TGCTTA 1830  
430 ProAspThrSerTrpSerProAla-----MetAlaSerThrSerLeuSer 445  
1831 AGAAAGAGACCATTAATAAACCTCTCTGCTAAGAAAAATATGATGTCCAAAGAGAACTTCA 1890  
446 GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThr 455  
1891 TCACAGAAAAACAGGAATTCGAAAGCGGTACTGATGTTAATATACATGTTAAATCT 1950

466 AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThrSer 484  
1951 AGAAAAAGCTCAAAATACTGATAAAACGCAACCACTCAAAAGCTGTTGAAATGTTTCC 2010  
485 AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerAsp 504  
2011 CGACTGAGTGAGCAGCAGCAGCAGCAGCAGCTCATCAGACTCTGAAAGTACGAGCAGT 2070  
505 Asp-----SerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGlu 521  
2071 GACTTAAGCTCTTCACAGCAGCAGTATTGTAATCAGAAATGTTCCCTAAGTTTACAGAA 2130  
522 MetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSer 541  
2131 GTAAAAACCAATGATTCTCTTCTAAAGAGCATGTAAGAAAAATGAAGAATGAATGCATA 2190  
542 ValProAsp-----HisPheLeuGluAspThrThrPro 552  
2191 CTGCTTGAAGGAAGAACAGCGCTCACAGATAGGATATTGTGCAAGACACACCTCT 2250  
553 Val---SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArg 571  
2251 GCCAATPACTACCTTGTTCATCAGACACACACCTTCACATGTAATGCCAACCAATCACCAC 2310  
572 GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
2311 CAATTAGCA-----TTT 2322  
592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThr-----GlnLeuLeu 609  
2323 AATTATCAAGAAATTAGAACATTTACAGACTGTGAAAAACATTTACCTTTACAAATTCG 2382  
610 ValPro-----TyrLeuArgSerAsnLeuThrGlyPhe----- 620  
2383 CCTCCTCAGGTGATTCTGAAACAGCTCTCAATGGCAATACCTGATCATCATCTGCT 2442  
621 -----LysGlnLeuGlu 624  
2443 GATAGTGACAAACGATGTTAGAACTGTAATGCAAGCTCTGTACAGAGGATATAAAG 2502  
625 IleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSer 644  
2503 ATTAAGAAAT-----GCAGATTATGGAAGTTTAGGCAACCA 2541  
645 Val---ProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAla 663  
2542 GTGAACCATCAGGTGTAATGAATCCCTCAGATGAGCTTTCACCAATTTAGAAAAAGCA 2601  
664 Ala-----AlaGlnGlnLeu-----HisLeuGluLeu 672  
2602 GCATAGAAAAAGAAAGTAAAGCTCGGACACAGGAACTCATACGGAAGCATTTGGAACAA 2661  
673 AspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAla 692  
2662 AATCAAGAAACTAAAGCATCTCAAGAAATCAGAGGATCTTGGGAATGATGACT 2721  
693 CysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
2722 GTAGAATCTTTTCAATAATAAATAAACAACAGTCTCTGGAGAGAGCAG 2772

RESULT 9  
US-09-392-714-4  
; Sequence 4, Application US/093927144  
; Patent No. 6686147  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew J.  
; APPLICANT: Gure, Ali O.  
; APPLICANT: Williamson, Barbara  
; APPLICANT: Chen, Yao-Tseng  
; APPLICANT: Old, Lloyd J.  
; TITLE OF INVENTION: Cancer Associated Antigens and Uses  
; TITLE OF INVENTION: Therefor  
; FILE REFERENCE: L0461/7062

; CURRENT APPLICATION NUMBER: US/09/392,714A  
 ; CURRENT FILING DATE: 1999-09-09  
 ; EARLIER APPLICATION NUMBER: PCT/US98/14679  
 ; EARLIER FILING DATE: 1998-07-15  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 3106  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-392-714-4

## Alignment Scores:

Pred. No.: 0.000136 Length: 3106  
 Score: 144.50 Matches: 150  
 Percent Similarity: 34.23% Conservative: 116  
 Best Local Similarity: 19.31% Mismatches: 321  
 Query Match: 3.51% Indels: 191  
 Db: 4 Gaps: 32

US-10-007-270-2 (1-797) x US-09-392-714-4 (1-3106)

Qy 16 LeuGlnValGlnGlyThrLysAspIleSerIleAsnIleThrHisSerGluThrLysAsp 35  
 Db 766 CTGCACTTCAGCTTAACCAAGTAGTGAATTTCTCAACATTCACAGAA-AAATCA 824  
 Qy 36 Ile-----AspAsnProProArgAsn----- 42  
 Db 825 GTGGCACTGCCACCTATAAAGAAATATGCAAGAAATGTTTGGCAGATTCTCAGCAA 884  
 Qy 43 -----GluThrThrGluSerThrGluLysMetThrLysMetSerThrMet 57  
 Db 885 CAATATAATGTTGGAGAGCTGTTAAAGTAACAGCAATTAAGGCACCTAGTAGAGATT 944  
 Qy 58 ArgArgIlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePhe---ProThr 76  
 Db 945 CTTAAAGAAATGCTTGCAAGAACATTTTTCATATGTCATGGCCCTTTATAATCCTGTT 1004  
 Qy 77 GlyLysValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyr 96  
 Db 1005 GACGTTAATGCTTTG-----GGACTCCATAACTACTATGACGTTGTCAAAATCCG 1055  
 Qy 97 TyrArgLeuArgValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArg 116  
 Db 1056 ATGATCTTGGAACTATTAGAGAAATG----- 1085  
 Qy 117 IleProAspThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCys 136  
 Db 1086 -----GATAACCAAGAAATATAAGATGCACTACTATTTCGGCA----- 1124  
 Qy 137 LeuPheAspIleGlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGln 156  
 Db 1125 -----GATGTTAGATTAATGTTTCATGAATGCTACAAGTAC----- 1160  
 Qy 157 ArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeu 176  
 Db 1161 -----AATCTCCAGATCAGAAAGTGTGACATGCGCAAGATGCTT 1202  
 Qy 177 GlyGluProGlyThrIleValIleSerThrAspValAlaAsnValSerLeuGlyPro 196  
 Db 1203 CAGGAT-----GTTTCGAACGCATTTTTCRAAGATCCCGATTGAACCT 1247  
 Qy 197 PheProLeuThrProAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAsp 216  
 Db 1248 GTTCAGAGTAGCTTTATGTTTACATCAAAACAGATATACAGAAACCACTGGTAGAGAG 1307  
 Qy 217 ThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgVal 236  
 Db 1308 AACACTAATGAAGCCCTCTGTAAGGGAACCTTCTGATGATTCGAAGATGAGCGAGTT 1367  
 Qy 237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256  
 Db 1368 -----AAGCGTCTTGAAGAGCTTCAGGAGCAGCTTAA 1400

Qy 257 ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLys 276  
 Db 1401 GCTGTACATCAACAGCTCCAGGTTTGTCCCAAGTACCTTTCCGTAAGCTAAATAAAG 1460  
 Qy 277 LeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysLysLysAspGly 296  
 Db 1461 AAAGAGAAGTCTAAAG-----GAAAGAAAGAAAGAAAGGTTAAT 1502  
 Qy 297 SerSerSer-----ThrGluMetGlnLeuThrAlaIlePheLys 309  
 Db 1503 AACAGCAATGAAATCCAAAGAAATGTTGAGCAATAGAGCTTAAGGAAAGTCCAG 1562  
 Qy 310 ArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLys 329  
 Db 1563 AGAAAT-----CAGCCAAAGAAAGGAAACACAGTTCATTGGT----- 1601  
 Qy 330 IleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyr 349  
 Db 1602 CTAATAATCTGAAGAT-----GAAGATAATGCTAAACCTATGAACCTAT 1643  
 Qy 350 LeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeuGluGluGlnSerLeu 369  
 Db 1644 -----GATGAGAAAGGCGAGTTAAGTCTGAATATAAAACAACTCCCTCGAGAT 1691  
 Qy 370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
 Db 1692 AAACCTGGCGAGTA-----GTTCAATAATATCAATCAAGAGAGCTTCTCTGAGCAAT 1745  
 Qy 390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
 Db 1746 TCCAACTCCTGATGAGATAGATAGACTTTGAAACACTG---AAAGCATCAACACTAAGA 1802  
 Qy 410 ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeu 429  
 Db 1803 -----GAATTAGAAATAATGTTTCGGCA-----TGTCTA 1832  
 Qy 430 ProAspThrSerTrpSerProAla-----MetAlaSerThrSerLeuSer 445  
 Db 1833 AGAAAGACCATTAACACCTCTGCTAAGAAATAATATGATGTCCAAAGAAAGAACTTCA 1892  
 Qy 446 GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThr 465  
 Db 1893 TCACAGAAAAACAGGAATGGAAGGCTTACTGGATGTTAATAATCACTTAATTTCT 1952  
 Qy 466 AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThrSer 484  
 Db 1953 AGAAACCTCAACCAAAATCTGATAAAACGCAACCATCCAAAGCTGTGAAAATGTTTCC 2012  
 Qy 485 AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAsp 504  
 Db 2013 CGACTGAGTGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2072  
 Qy 505 Asp-----SerArgSerAlaGlyGlyGluAspMetValArgHisLeuAspGlu 521  
 Db 2073 GACTTAAGCTTTCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2132  
 Qy 522 MetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSer 541  
 Db 2133 GTAAACCAAAATGATCTCTCTTCTTAAAGAGCATGTAAGAAATAAGAAAGTAATGATG 2192  
 Qy 542 ValProAsp-----HisPheLeuGluAspThrThrPro 552  
 Db 2193 CTGCTGAGAGGAGAAACAGGCGTCACAGATGAGATTTGTGTGCAAGACACACCTCT 2252  
 Qy 553 Val---SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArg 571  
 Db 2253 GCCAATACTACCTTGTTCATCAGACCCACACCTTCACATGTAATGCCAACCAATCACCAC 2312  
 Qy 572 GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
 Db 2313 CAATTAGCA-----TTT 2324



Db 1984 TACCTGTACATACATTTTACCAAGAGAGACGGGGTACTCTCCATTACAGATACAGT 2043  
Qy 318 ProAlaSerAspLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337  
Db 2044 TCATCCTCAGACATTTGTGGAGAGCTCACTTCTATATAAATCTCAAACTCTTCACAT 2103  
Qy 338 GlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArg 357  
Db 2104 TCAGAGTATCTCTCTTCTCATGCTCAG-----ACTGAGAGAGTAAC 2148  
Qy 358 LeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThr 377  
Db 2149 ATCTCATCTATACGGGGAATATGTCAGCCCTTCTACTAGTCGCCAGTTCTGCATACA 2208  
Qy 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396  
Db 2209 TCAACCTTCCCTCCTACACCCCACTTAATATGCGCAACACTCGGTGTTCTCGGAC 2268  
Qy 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409  
Db 2269 ACTGATGCTGAGTTGTTAGTGACTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 2328  
Qy 410 -----ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu 426  
Db 2329 TCTTCAGGCGCT 2373  
Qy 427 His-----GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThr 442  
Db 2374 CATTTATTTTCATCAATTTTACCATCAACAGGGCTCTGTGCATCTACTAAAGTCTACC 2433  
Qy 443 SerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462  
Db 2434 TCTGATGATCACCACCA-----TGGTCTCTCTCACCATCACCCTTTACAGTATCC 2484  
Qy 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482  
Db 2485 TTAACGATCATCTACTCTGCCC-----CCACTTCTGCTCACAACAACCTTGCCA 2535  
Qy 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSer 502  
Db 2536 CAGTCATCTTACCCCTGCTGTCGCCAGGCA-----AGGAGAGCTCTCTGTGACT 2586  
Qy 503 SerAspAspSerArgSerSerAlaGlyGluAspMetValArgHisLeuAspGluMet 522  
Db 2587 TCATTTTCAGATCAACATGACATCATTCATGCAATGCTCCATAGTAGTCAAACTGCA 2646  
Qy 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
Db 2647 GACCTTAAGCCAGACACCCACACCAAGAGAAAGTCAATACAGAAATCAAACTCACA 2706  
Qy 539 ---TyrValSerValProAspHisPheLeuGluAspThrProValSerAlaLeuGln 557  
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Qy 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValPhePhe 577  
Db 2767 CCATCCTTAACAGAGCTCTCCACA-----GAGCAAAACCTTCCAGCCACA 2811  
Qy 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594  
Db 2812 AGCACCACCTTAGCACAAATGCTCCCACTTTCACACTCATCTCTGAGACCTCTCAG 2871  
Qy 595 -----SerLeuGluTyrArgAlaLeu 601  
Db 2872 CCTCTATGACCATCTCGGCACCCCTGTCAAGCAGCAGCATCTCTGTGCTGGCCCTATA 2931  
Qy 602 GluGlnGlnPheThr-----GlnLeuLeuValPro 611  
Db 2932 GCCGTACAGATCAGCTGGAAGAACAGCTCTCGCTGACCCATCTGAAATACTAGTTCT 2991  
Qy 612 TyrLeu-----ArgSerAsnLeuThrGlyPheGlnLeuGluIleLeuAsnPheArg 629

Db 2992 CAAATCTCAACAGAGGTGGCATCAGCACAGAAAGAACCGAGTGTATTGTGGATGTCTACC 3051  
Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
Db 3052 ACTGGATTGATCCTTTGACCACTGTACCCACATCAGCAAAAGAAATGACCACAAAGCTT 3111  
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaIleGlnLeuHis 669  
Db 3112 -----GCGGTTACAGCAGATACAGCCAGCT----- 3138  
Qy 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684  
Db 3139 -----TCAGTCTCCCTCGGAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 3186  
Qy 684 ----- 684  
Db 3187 ACGGCTGAAGACTTGGCTCCCAATCTGCCACCTTTGTCTTCAGAGCAGCACAGTCA 3246  
Qy 685 -----AlaAspProCysLysPheLeuAlaCysGlyGlu 695  
Db 3247 CCACACACTGCTCTTTCAGCCTCAGTCAACAGCTGTGTGTGAAACCTTGTCTTCCAC 3306  
Qy 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715  
Db 3307 AATGGGAATGGTCTCGCAGACACACAGCCGCTGCTACCTGCGAGGTGCCGCTTCC 3366  
Qy 716 TyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCys-----Gly 731  
Db 3367 TGG-----CAGGGGATGATTCAGTGTGGATGAATGAGTGTCTGCGAACCCCTGC 3420  
Qy 732 ProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuPro--- 750  
Db 3421 CCATCCACAGCCAGCTGCAACAATACTCAGGATCCTTTATC---TGCAATGCCCGTT 3477  
Qy 751 -----AspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGln 766  
Db 3478 GGGTACCATGTGGAAAAAGGATATGCAATTTGGTTAGAACCTTCTGTGACAGATTAAA 3537  
Qy 767 AsnGlnGlnAsn-----AsnLysValIleSerLysArgAsnSerGluLeuLeuThrVal 784  
Db 3538 TTAAGAGAACTTTCTTAATACAACTGTGGAAAAA---CATTCAGACCTACAGAGTT 3594  
Qy 785 GluTyrGlu 787  
Db 3595 GAAATGAG 3603

RESULT 11  
US-08-599-654-7  
; Sequence 7, Application US/08599654  
; Patent No. 5882925  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/599,654  
; FILING DATE: 09-FEB-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573

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/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/386,844
/ FILING DATE: 10-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CORUZZI, LAURA A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7853-041
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864
/ TELE: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6407 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cDNA
US-08-599-654-7

Alignment Scores:
Pred. No.: 0.00102 Length: 6407
Score: 141.50 Matches: 164
Percent Similarity: 31.91% Conservative: 105
Best local Similarity: 19.45% Mismatches: 356
Query Match: 3.44% Indels: 219
DB: 2 Gaps: 34

US-10-007-270-2 (1-797) x US-08-599-654-7 (1-6407)
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DB 1275 TGGAGAACATCAGCTTGCAGCAGCTCTGAGGTGCAAAATGGAAGTCCCATGTCTCAGAC 1334
QY 114 LeuAspArgIleProAspThrGlyGluTrpGlnAspTrpValSerIleCys----- 130
DB 1335 TGAGACTGTCTAGGTGAGTGCAGCCATGAGAGGTGGAGAGATCACTGCACACTGGCT 1394
QY 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyAsn----- 143
DB 1395 CTTGACCAACAGCAACATCTGCAGATGTGACA--GGAAGCTGTGCTTCATATCCTGAA 1452
QY 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154
DB 1453 GGTGTGAATGTTTCAGTGTGACCCAGTCTTCAGACTCTACTGTACAGTCTGGAGGAAGT 1512
QY 155 GlnGlnArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGlu-- 173
DB 1513 CACACAGCATTTGGGAGATAGGAGTTATTCAGAGTCTTCATCATCTTCTCGGAAGC 1572
QY 174 -----LysThrLeu-----GlyGluProGly 180
DB 1573 TTGAATTCATCAGCACACACGTGGAGAGAGTTCAACCTTGGAGACAGCCGAGAGCCAGGC 1632
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
DB 1633 CAAGCACTAGTGTGACAGTTCGCCAATGCAGAGCAGGAGTCTGGGGTCCCTCTCTC 1692
QY 201 ProAspAspThrLeuLeu-----AsnGluIleLeuAspAsnThr 213
DB 1693 GGCACCCACACCTTGGCTACTGTCTACTGTGAAACGGGGAACGCACACTCGCGTCTGTCA 1752
QY 214 LeuAsnAspThrLysMetProThrThrGlu----- 223
DB 1753 CTCACCAACACAGCATGACGACACTTCTGGGGAAGCAGCAGCCCTGAGCGGGCCATG 1812
QY 224 ---ArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeu 242
DB 1813 CCCCAAGAAACAGAGGGTGCCTCTCTGCAC----- 1842
QY 243 ValAsnGlnLysPheLeuAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu 262
DB 1842 AGCACCACCTTAGCACAATAATGTCTCCAACTTTCCAACTTCTGGAAGACCTCTCAG 2871

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DB 1843 -----GTAAACGTGACGGAGACATGGGCTGGTCTCAGCGTCACTG 1884
QY 263 AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLeuProGlyPheLysLys 282
DB 1885 GCGCGCTCCAGTGCATCGGAGTCTGGGATT-----AGCTACGTCGTCAA 1929
QY 283 IleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThrGluMet 302
DB 1930 GTGCGTGGCAGCAGTATTGAACAAGAGCTTCACGGACCCACACAGCACACC----- 1983
QY 303 GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317
DB 1984 TACCTGTCTACTCTTCCACAAAGAGAACCGGGGTACTGTCCATTACAGATAACAGT 2043
QY 318 ProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337
DB 2044 TCATCTCAGACATTGTGGAGAGCTCAACTCTTATATTAAATCTCAAACTCTTCACAT 2103
QY 338 GlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArg 357
DB 2104 TCAGAGTATTCTCTCTTTCTCATGCTCAG-----ACTGAGAGAAAGTAA 2148
QY 358 LeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThr 377
DB 2149 ATCTCATCTATGACGGGAATATCTCAGCCTTCTACTGAGTCGCCAGTCTTCGATACA 2208
QY 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396
DB 2209 TCCAACCTTCGCTCTACACACCCACCATTAATATGCGGAACACTCCGTTCTTCGAC 2268
QY 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409
DB 2269 ACTGATGTGAGTTTGTAGTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328
QY 410 -----ProGluLeuProValGluProGlnLeuGluThrValAspGlyValaGlu 426
DB 2329 TCTTCAGGCGCTCTCTTGGCT-----CTGCCCTCTGTGTCTCAATCCAC 2373
QY 427 His-----GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThr 442
DB 2374 CATTTATTTCATCAATTTTACCATCAACAGGGGCTCTGTGCATCTACTAAAGTCTACC 2433
QY 443 SerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462
DB 2434 TCTGATGATCCACACCA-----TGGTCTCTCTCACCATCACCTTTTACCAGTATCC 2484
QY 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482
DB 2485 TTAACGACATCTACATCTGCC-----CCACTTTCTGTCTCACAAACACCTTGCCA 2535
QY 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSer 502
DB 2536 CAGTCATCTTCTACCCCTGTCTGCCAGGGCA-----AGGGAGACTCTCTGTGACT 2586
QY 503 SerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522
DB 2587 TCATTTTCAGACATCAACATGACATCATCATGACATGCTCCATAGTAGTCAAACTGCA 2646
QY 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538
DB 2647 GACCTTAAGAGCCAGCAGCAGCCACACCAAGAGAAAGTCATTACAGAATCAAGTCAACA 2706
QY 539 ---TyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557
DB 2707 AGCTTGGTGTCTCTGCCAGAGTCCACCAAGTGTAAACAACTTCCTTTTGGCT 2766
QY 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValPhePhe 577
DB 2767 CCATCTCTTAACAGAGTCTCTCCACA-----GAGCAAAACCTTCCAGCCACA 2811
QY 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594
DB 2812 AGCACCACCTTAGCACAATAATGTCTCCAACTTTCCAACTTCTGGAAGACCTCTCAG 2871

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QY 595 -----SerLeuGluTyrArgAlaLeu 601
Db 2872 CCTTTATGACACTCTCTGGCACCTGTCAAGCAGCATCTCTGGTCACTGGCCCTATA 2931
QY 602 GluGlnGlnPheThr-----GlnLeuLeuValPro 611
Db 2932 GCCGTACAGACTACAGCTGGAAACAGCTCTCGTGACCCATCTCGAACTAGTTCCT 2991
QY 612 TyrLeu-----ArgSerAsnLeuThrGlyPheLysGlnLeuGluLeuLeuAsnPheArg 629
Db 2992 CAATCTCAACAGAGGTGGCATCAGACAGAAAGGAAACCGAGTGTGGATGCTTACC 3051
QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649
Db 3052 ACTGGATTGATCCCTTTGACAGTGTACCCACATCAGCAAAAGAAAGTACACCAAGCTT 3111
QY 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669
Db 3112 -----GGCGTTACAGCAGAGTACAGCCAGCT----- 3138
QY 670 LeuGluLeuAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684
Db 3139 -----TCAGTTCCTCCGGAACATCTCTCTCCCAACCAACAGTGTGTTC 3186
QY 684 ----- 684
Db 3187 ACGCTGAAGACTGGCTCCCAATCTGCCACCTTTGCTGTTCAGAGCAGCACAGTCA 3246
QY 685 -----AlaAspProCysLysPheLeuAlaCysGlyGlu 695
Db 3247 CCAACAACACTGTCTCTTCAGCCTCAGTCAACAGCTGTCTGTGAACCTTCTCTTCAC 3306
QY 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715
Db 3307 AATGGCAATCGTTCGACACACACACCGCGGTGGTACCAGTGCAGGTGCCCGCTTC 3366
QY 716 TyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCys-----Gly 731
Db 3367 TGG-----CAAGGGGATGATTGAGTGTGGATGTAATGAGTGTCTGTGAACCTCTC 3420
QY 732 ProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuPro--- 750
Db 3421 CCATCCACAGCCAGTGCACATATCTCAGGATCCCTTATC---TGCAATGCCCGGT 3477
QY 751 -----AspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGln 766
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QY 767 AsnGlnGlnAsn-----AsnLysValIleSerLysArgAsnSerGluLeuThrVal 784
Db 3538 TTAAGAGAACTTTCTTAATACAACTGTGGAATAA---CATTCAGACCTACAAGAAGTT 3594
QY 785 GluTyrGlu 787
Db 3595 GAAATGAG 3603
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## RESULT 12

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US-08-944-868A-7
; Sequence 7, Application US/08944868A
; Patent No. 6018025
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDWARDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,868A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,654
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6407 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-944-868A-7
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## Alignment Scores:

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Pred. No.: 0.00102 Length: 6407
Score: 141.50 Matches: 164
Percent Similarity: 31.91% Conservative: 105
Best Local Similarity: 19.45% Mismatches: 356
Query Match: 3.44% Indels: 219
DB: 3 Gaps: 34
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US-10-007-270-2 (1-797) x US-08-944-868A-7 (1-6407)

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Db 1275 TGGGAACATCAGCTTGCACAGCTCTGAGGTGCAAAATGGAAGTCCCATGCTCAGAC 1334
QY 114 LeuAspArgIleProAspThrGlyGluTyrGlnAspTrpValSerIleCys----- 130
Db 1335 TGAGACTGTGTCTAGGTGAGTCCGCCATCAGAGGTGGAGAGATCACTGCACACTGGCT 1394
QY 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsn----- 143
Db 1395 CTTGACCAACAGACACAACATCTGCAGATGTGACA--GGAAGCTCTGCTTCATATCCTGAA 1452
QY 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154
Db 1453 GGTGTGAATGTTCAAGTGTGACCCAGTCTTCAGACTCTACTGTACAGTCTGGAGGAAGT 1512
QY 155 GlnGlnArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGlu--- 173
Db 1513 CACACAGATTGGGAGATAGGAGTTATTCAGAGTCTTCATCTACATCTCTCTCGAAGC 1572
QY 174 -----LysThrLeu-----GlyGluProGly 180
Db 1573 TTGAATTCATCAGCACCCAGTGGAGAACGTTCAACCTTGGGAAGACAGCCGAGCAGGC 1632
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db 1633 CAAGCACTAGGTGACATTCGCGCAATGCAGAGCAGGACTTCTGGGGTGCCTCTCTC 1692
QY 201 ProAspAspThrLeuLeu-----AsnGluIleLeuAspAsnThr 213
Db 1693 GGCACCCACACCTTGGCTACTGTCACTGGAAACGGGGAACGCACACTGCGGTCTGTCA 1752
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QY 214 LeuAsnAspThrLysMetProThrThrGlu----- 223  
DB 1753 CTCACCAACACCATGACGACGACTTCTGGGAAGCAGCAGCCCTGCAGCGCCCATG 1812  
QY 224 ---ArgGluThrGluPheAlaValLeuGluGluGlnAArgValGluLeuSerValSerLeu 242  
DB 1813 CCCCAAGAAACAGAGGGTCTCTCGCAC----- 1842  
QY 243 ValAsnGlnLysPhePheAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu 262  
DB 1843 -----GTAAACCTGACCGACGACATGGCCCTGGTCTCTCAGGTCACTG 1894  
QY 263 AlaGlyLysSerGlnLeuGlnMetGlnLysLysLeuProGlyPheLysLys 282  
DB 1885 GCCGCTCCAGTGCATCGGAGTCTGGGATT-----AGTACGGTCAA 1929  
QY 283 IleHisValLeuGluPheArgProLysLysGluLysAspGlySerSerThrGluMet 302  
DB 1930 GTGCGTGGCACAGCTATTGAACAAAGAGACTTCCAGCGACACACAGCACACC----- 1983  
QY 303 GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317  
DB 1984 TACCTGTCTATCTCTTACCAAGAGAGAACGGCGGTACTGTCTTACGATTAACAGT 2043  
QY 318 ProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337  
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QY 338 GlyThrMetGluGluAspLysGlnProGluLeuTyrLeuThrAlaThrAspLeuLysArg 357  
DB 2104 TCAGAGTATTCCTCTTCTCATGCTCAG-----ACTGAGAGAAGTAAC 2148  
QY 358 LeuIleSerLysAlaLeuGluGluGlnGlnSerLeuAspValGlyThrIleGlnPheThr 377  
DB 2149 ATCTCATCTGACGGGAATATGCTCAGCCTTCTACTGAGTCGCCAGTTCGCATACA 2208  
QY 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396  
DB 2209 TCCAACTTCCTGCTCACACCCCAACCATTAATATGCCGAACACTTCGGTTGTTCTGGAC 2268  
QY 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409  
DB 2269 ACTGATGTGAGTTGTTAGTACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328  
QY 410 -----ProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlu 426  
DB 2329 TCTTCAGGCGCTCTCTTGCT-----CTGCCCTCTGTGTCACAATCCAC 2373  
QY 427 His-----GlyLeuProAspThrSerTyrSerProProAlaMetAlaSerThr 442  
DB 2374 CATTTATTTTCATCAATTTTACCATCAACCGGCGCTCTGTGCATCTACTAAAGTCTACC 2433  
QY 443 SerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462  
DB 2434 TCTGATGATCCACACCA-----TGGTCTCTCTCACCATCACCCTTTACAGTATCC 2484  
QY 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482  
DB 2485 TTAACGACATCTACATCTGCC-----CCACTTCTGTCTCACAAACCACTTGCCA 2535  
QY 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSer 502  
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QY 503 SerAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522  
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QY 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
DB 2647 GACCTTAAAGCCAGAGCAGCCCAACCAAGAGAAAGTCAITACAGAAATCAAAAGTCACCA 2706

QY 539 ---TyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557  
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DB 2767 CCATCTTAACAGAGTCTCCACA-----GAGCAAAACCTTCCAGCCACA 2811  
QY 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594  
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QY 595 -----SerLeuGluTyrArgAlaLeu 601  
DB 2872 CCTCTTATGACCACTCTCTGCGACCCCTGTCAAGCAGCATCTCTGTCTACCTGCGCCTATA 2931  
QY 602 GluGlnGlnPheThr-----GlnLeuLeuValPro 611  
DB 2932 GCGGTACAGACTACAGCTCGAAAAACAGCTCTCGTACCCATCTCTGAATATAGTCTCT 2991  
QY 612 TyrLeu-----ArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
DB 2992 CAATCTCAACAGAGTGGCATCAGCACAGAAAGAACCGAGTGATTTGGATGCTTACC 3051  
QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
DB 3052 ACTGGATTGATCCTTTGACCACTGATCCACATCAGCAAAAGAAATGACCAAAAGCTT 3111  
QY 650 ThrLysAlaValIleGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
DB 3112 -----GGCCTTACAGAGATGACGCCAGCT----- 3138  
QY 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684  
DB 3139 -----TCAGTTTCCCTCGGAACATCTCTCTCTCCCAACCAACACAGCTTGTTC 3186  
QY 684 ----- 684  
DB 3187 AGCGTGAAGACTTGCTCTCCAAATCTGCCACTTGTGCTTTCAGAGCAGCACAGTCA 3246  
QY 685 -----AlaAspProCysLysPheLeuAlaCysGlyGlu 695  
DB 3247 CCAACAACACTGCTCTCTTCAGCCTCAGTCAACAGCTGTGTGTGAACCTTGTCTTCA 3306  
QY 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715  
DB 3307 AATGGCAATGGTTCGCAGACACACAGCCGCTGCTACCACTGCAGGTGCCCGCTTCC 3366  
QY 716 TyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCys-----Gly 731  
DB 3367 TGG-----CAAGGGATGATTGAGTGTGAATGAATGAGTGTCTGCAACCCCTG 3420  
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RESULT 13

US-08-944-423A-7

; Sequence 7, Application US/08944423A

; Patent No. 6020463

; GENERAL INFORMATION:

APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,423A  
FILING DATE: 06-OCT-1997  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: JUN-07-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
US-08-944-423A-7

Alignment Scores:  
Pred. No.: 0,00102 Length: 6407  
Score: 141.50 Matches: 164  
Percent Similarity: 31.91% Conservative: 105  
Best Local Similarity: 19.45% Mismatches: 356  
Query Match: 3.44% Indels: 219  
DB: 3 Gaps: 34

US-10-007-270-2 (1-797) x US-08-944-423A-7 (1-6407)

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QY 114 LeuAspArgIleProAspThrGlyGluTyrGlnAspTrpValSerIleCys----- 130  
DB 1335 TGAGACTGTGTCTAGGTGAGTCGCGACCCATGAGAGGTGGAGATCACTGCACACTGGCT 1394  
QY 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsn----- 143  
DB 1395 OTTGACCAACAGCACAACATCTGCAGATGTGACA--GGAACTCTGCTTCATATCCTGAA 1452  
QY 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154  
DB 1453 GGTGTGAATGCTTCAAGTGTGACCCAGTCTTCAGACTCTACTGTACAGTCTGGAGGAAGT 1512  
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DB 1633 CAAGCACTAGTGACAGTTCGCCCAATGACAGAGGACAGGACTTCTGGGTGCGCTCTCTC 1692  
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DB 1813 CCCCAAGAAACAGAGGTGCTCTCTGAC----- 1842  
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DB 2209 TCCAACCTTCGCTCTACACACCCACCATTAATATGCGGAACACTTCGTTGTTCTGGAC 2268  
QY 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409  
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QY 443 SerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462  
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Qy 503 SerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522  
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Qy 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
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Db 2812 AGCACAACCTTAGCAAAATGTCTCCAACTTTCACAACCTACCATCTCGAAGACCTCTCAG 2871  
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Db 2872 CTTCTTATGACACTCTCTGGACCTGTCAAGCAGCATCTCTGGTCACTGGCCCTATA 2931  
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Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
Db 3052 ACTGGATTGATCCCTTTGACAGTGTACCCATCATGCAAAAGAAATGACCACAAGCTT 3111  
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaAlaGlnLeuHis 669  
Db 3112 -----GGCGTTACAGCAGTAGTACGCCCGCT----- 3138  
Qy 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684  
Db 3139 -----TCAGTTCCCTCGGAACATCTCTTCTCCCAACACACAGTTGTTTCC 3186  
Qy 684 ----- 684  
Db 3187 AGGCTGAAGACTTGGTCCCAATCTGCCACTTTGCTTTTCAGAGCAGCAGCAGTCA 3246  
Qy 685 -----AlaAspProCysLysPheLeuAlaCysGlyGlu 695  
Db 3247 CCAACAACACTGTCTCTTCAGCCTCAGTCAACAGCTGTGTGTGAACCTTGTCTTCC 3306  
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Db 3307 AATGGCGAATGGTTCGACAGCAACACCGCGGTGTACCTACCTGCGAGTGGCGGCTTCC 3366  
Qy 716 TyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCys-----Gly 731  
Db 3367 TGG-----CAAGGGGATGATTGAGTGGGATGTGAATGAGTGGCTGTGCAACCCCTGTC 3420  
Qy 732 ProGlyThrLysGluCysGluValLeuGlnGlyLysGlyValProCysArgLeuPro--- 750  
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Qy 751 -----AspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGln 766  
Db 3478 GGGTACCAGTTGGAAAAAGGGATATGCAATTTGGTTAGAACCTTCTGTCAGCAGATTAA 3537

Qy 767 AsnGlnGlnAsn-----AsnLysValIleSerLysArgAsnSerGlnLeuLeuThrVal 784  
Db 3538 TTAAGAGAACTTTTCTTAATACAACCTGTGGAATAA---CATTCAGACCTCAAGAAGTT 3594  
Qy 785 GluTyrGlu 787  
Db 3595 GAAATGAG 3603  
RESULT 14  
US-08-944-496-7  
Sequence 7, Application US/08944496  
Patent No. 6124433  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,496  
FILING DATE: 06-OCT-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
US-08-944-496-7  
Alignment Scores:  
Pred. No.: 0.00102 Length: 6407  
Score: 141.50 Matches: 164  
Percent Similarity: 31.91% Conservative: 105  
Best Local Similarity: 19.45% Mismatches: 356  
Query Match: 3.44% Indels: 219  
DB: 3 Gaps: 34  
US-10-007-270-2 (1-797) x US-08-944-496-7 (1-6407)  
Qy 97 TyrArgLeuArgValCysGlnGlu-----AlaValTrpGluAlaTyrArgIlePhe 113  
Db 1275 TGGAGAACATCATCAGCTTGGCCAGCAGCTCTGAGGTGCAAAATGGAAGTCCCATCTCTCAGAC 1334

QY 114 LeuAspArgIleProAspThrGlyGluTyrGlnAspTrpValSerIleCys----- 130  
Db 1335 TGAGACTGTGCTAGGTCAGTCGACCATGAGAGGTGGAGATCACTGCACACTGGCT 1394  
QY 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsn----- 143  
Db 1395 CTTGACCAACAGACACACATCTGCAGATGTGACA--GGAAGCTGTGCTTATATCTGAA 1452  
QY 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154  
Db 1453 GGTGTGAATGCTCAGTGTGACCCAGTTCTTCAGACTCTAGTACAGTCTGGAGGAAGT 1512  
QY 155 GlnGlnArgIleLysGlnAspSerPheProAspArgLysAspGluIleSerAlaGlu--- 173  
Db 1513 CACACAGATTGGAGATAGAGATTATTCAGAGTCTTCATCTACATCTTCTCGAAGC 1572  
QY 174 -----LysThrLeu-----GlyGluProGly 180  
Db 1573 TTGAATTTCATCAGCACACACGTGGAGAAGCTTCAACCTTGAAGACAGCCGAGAGCCAGGC 1632  
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
Db 1633 CAGCACTAGGTGACAGTTCGCCAATGCAGAGACAGACTTCTGGGGTGCCTCTCTC 1692  
QY 201 ProAspAspThrLeuLeu-----AsnGluIleLeuAspAsnThr 213  
Db 1693 GGCACCCACACCTTTGGTACTGTCTCACTGGAACGGGAACGCCACACTGCGGTCTGTCAAC 1752  
QY 214 LeuAsnAspThrLysMetProThrThrGlu----- 223  
Db 1753 CTCACCAACACAGCATGAGCACACTTCTGGGAAGCAGCGCCCTGCGAGCGGCATG 1812  
QY 224 --ArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeu 242  
Db 1813 CCCCAAGAAACAGAGGTGCTCTCTGCAC----- 1842  
QY 243 ValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu 262  
Db 1843 -----GTAACGTGACGAGCAGCATGGCGCTGTCTCACGCTCACTG 1884  
QY 263 AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys 282  
Db 1885 GCGCCTCCAGTGCATCGGAGTCGCTGGGATT-----ACGTAGGTCAA 1929  
QY 283 IleHisValLeuGlyPheArgProLysLysGlnLysAspGlySerSerThrGluMet 302  
Db 1930 GTGCGTGCACAGCTATTGAAACAAGGACTTCCAGCGCACCACACAGCACACACC- 1983  
QY 303 GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317  
Db 1984 TACCTGTCTACTCTTTCACAAAGGAGAACGGCGCTTACTGTTCATTACAGATAACAGT 2043  
QY 318 ProLaserAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337  
Db 2044 TCATCCTCAGACATGTGGAGCTCACTCTTATTATTAATCTCAAACTCTTCACAT 2103  
QY 338 GlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArg 357  
Db 2104 TCAGAGTATTCCTCTTCTCTCATGCTCAG-----ACTGAGAGAAGTAAC 2148  
QY 358 LeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThr 377  
Db 2149 ATCTATCTATGACGGGAATATGCTCAGCTTCTACTAGTCGCGCAGCTTCGCATACA 2208  
QY 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396  
Db 2209 TCCAACTTCGCTCTACACACCCACCATTAAATGCGGAACACTTCGGTGTCTTGAC 2268  
QY 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409  
Db 2269 ACTGATGTGAGTTGTTAGTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328

QY 410 -----ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu 426  
Db 2329 TCTTCAGGCGCTCTCTTGCCT-----CTGCCCTCTGTGTCAAACTCCAC 2373  
QY 427 His-----GlyLeuProAspThrSerTrpSerProAlaMetAlaSerThr 442  
Db 2374 CATTTATTTTCATCAATTTTACCATCAACAGGCGCTCTGTGCATCTACTAAAGTCTACC 2433  
QY 443 SerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462  
Db 2434 TCTGATGATCCACACCA-----TGGTCTCTCCATCCATCCCTTTTACCATATCC 2484  
QY 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482  
Db 2485 TTAACGACATCTACATCTGCC-----CCACTTCTGTCTCACAAACACTTGCCA 2535  
QY 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProLaser 502  
Db 2536 CAGTCTCTTTCACCCCTGCTCTGCCAGGCA-----AGGAGACTCTCTGTGACT 2586  
QY 503 SerAspAspSerArgSerSerAlaGlyGluAspMetValArgHisLeuAspGluMet 522  
Db 2587 TCATTTACAGACATCAACATGACATCATTCATGACAATGCTCCATAGTAGTCAAACTGCA 2646  
QY 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
Db 2647 GACCTTAAGAGCCAGACGCCACCCACCAAGAGAAAGTCATTACAGAATCAAAAGTCACCA 2706  
QY 539 ---TyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557  
Db 2707 AGCCTGGTGTCTCTGCCACAGAGTCCACCAAGGTGTAAACAACAACTCTCTTTGGCT 2766  
QY 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePhe 577  
Db 2767 CCATCTTAACAGAGTCTCTCCACA-----GAGCAACCCCTTCCAGCCACA 2811  
QY 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594  
Db 2812 AGCACAACCTTAGCAAAATGTCTCCAACTTTCACAACTACCATTTCTGAAGACCTCTCAG 2871  
QY 595 -----SerLeuGluTyrArgAlaLeu 601  
Db 2872 CCTCTTATGACCACCTCTGGCACCCTGTCAAGCACAGCATCTCTGGTCACTGGCCCTATA 2931  
QY 602 GluGlnGlnPheThr-----GlnLeuLeuValPro 611  
Db 2932 GCGGTACAGACTACAGCTGGAACACAGCTCTGCTGACCCCATCTCTGAAATACTAGTTCT 2991  
QY 612 TyrLeu-----ArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
Db 2992 CAAATCTCAAGAGGTGGCATCAGACAGAAAGAACCGAGTGATTGTGGATCTTACC 3051  
QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
Db 3052 ACTGGATTGATCCCTTTGACCACTGTACCACATCAGCAAAAGAAATGACCAAAAGCTT 3111  
QY 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
Db 3112 -----GGCGTTACAGCAGATACAGCCAGCT- 3138  
QY 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684  
Db 3139 -----TCAGTTTCCCTCGGAACATCTCTCTCTCCCAACCCACAGTGTGTTCC 3186  
QY 684 ----- 684  
Db 3187 ACGGTGAAGACTTGGCTCCCAATCTGCCACCTTTGTCTGTTCAGAGCAGCACACAGTCA 3246  
QY 685 -----AlaAspProCysLysPheLeuAlaCysGlyGlu 695  
Db 3247 CCAACAACACTGTCTCTTCAGCTCAGTCAACAGCTGTGTGTGAACCTTGTCTTCCAC 3306  
QY 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715

Qy	116	ArgIleProAspThrGlyGlyTyrGlnAspTrpValSerIleCysGlnGlnGluThrPhe	135
Db	391169	AAA-----GAAACACGGGGTTTACTATGATCCTTATGAGATACTGAATATGATATCTCC	391116
Qy	136	CysLeuPheAspIleGlyLeuAsn-----PheSerAsnSerGlnGluHisLeuAsp	152
Db	391115	CAACTCTTTGATGAAATGGGAATCCGTTGTTTGTATGAAAGCAAGAGAGATGAT	391056
Qy	153	LeuLeuGlnGlnArgIleLysGlnArgSerPheProAsp	165
Db	391055	TATTTA-----AAGTATGTTGGTAACCTGACATATGGTTCTTATGATGAAAAAT	391008
Qy	166	-----ArgLysAspGluIleSerAlaGluLysThrLeu	176
Db	391007	GGTAGTGGGTTTGATCTGGTTACTCTTGAAATGACACAGTGGATCTCCACTAAAGATCT	390948
Qy	177	GlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyPro	196
Db	390947	CAACCAACTGATGAAACATATGGTTTTCACATGAT-----	390912
Qy	197	PheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAsp	216
Db	390911	-----TTACCACCAAGAGTAAACCAACCTGAATCATGCTGGAAGATAACTATGCTTTGAT	390858
Qy	217	ThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGluGln-----	234
Db	390857	AACGATTTTACCACCAAGAGTAAACCAACCTGAA-----TCAGTTGAAGATAACTATGCT	390804
Qy	235	-----ArgValGluLeuSerValSerLeuValAsnGlnLys-----	246
Db	390803	TTTGATAACAGCTTACCACCAAGAGTAAACCAACCTGAATCAGTTGTGACCACTTCT	390744
Qy	247	-----PheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu	262
Db	390743	TCAGATGATTATTTTGCAAAACCAACCACTGATGAAATATGGTTTGATAACGACCTA	390684
Qy	263	AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys	282
Db	390683	CCA-----CCAGAAGTAAAA-----CCAGAAGTAAAA-----	390669
Qy	283	IleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThrGluMet	302
Db	390668	-----CAACTGAATCAGTTGTTGACCAACCTTCTTCAGATGAT-----	390630
Qy	303	GlnLeuThrAlaIlePheLysArgHiseralGluAlaLysSerProAlaSerAspLeu	322
Db	390629	-----CATTTTGCMAAACCAACCTGAATCAACACTGATAGC	390594
Qy	323	LeuSerPheAspSerAsn-----LysIleGluSerGlu	333
Db	390593	TCACGCTTTGACAGTGATTACTCAACCAACCTTGACCAACCTCTTTAGATGATCAT	390534
Qy	334	GluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThr	353
Db	390533	GTTTCAGTACAACCTTTTGATCACCATGAAGAGCTCAACCA-----	390495
Qy	354	AspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThr	373
Db	390494	-----GTTGCTGAAGAACAAAAATATTAATCAAGTTGGA-----	390462
Qy	374	IleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSer	393
Db	390461	-----TTTGATCAAGTTCAGCTAATCTT-----GATATAATAGAG	390426
Qy	394	GluLeu-----ProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu	412
Db	390425	GAAATACCAACCAACTGCTGAAAAAAGTAACTACTACTGATTTTGAA-----	390381
Qy	413	ProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro-----	431
Db	390380	-----AGTAACAAGCCCAAGTAGTTGAT-----AGTTACCAATTACCAATGAT	390336
Qy	432	ThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaPro-----	448

[illegible]

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QY 448 -----
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QY 449 ProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMet 468
Db 390215 CCA-----GTTTGAAGAAGTAGTTTCAATAAACAAGATAGTAGTTGAAACTAGTGACTTA 390162
QY 469 AlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAla 488
Db 390161 AATTCTGAATCTAATCTTTACTTGAAACCAACAAGATGCAACTAACAATGATTCATTA 390102
QY 489 IleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSer 508
Db 390101 AATTCTGAATTCATTCAACTTAAATAGTAATAGTGAACACTGCATCTGATGATGTCATTAT 390042
QY 509 SerAlaGlyGlyLeuAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528
Db 390041 GAAAGTAATCTGAACCAATTCATGACTATATAATTTGGAGTGATTTATCTCAATCAAC 389982
QY 529 AlaProSerGluVal-----ProGluLeuSerGluTyrValSerValProAsp--- 544
Db 389981 AGCAATAATTCGTTAGAGTCTGAACCTGTTAAGTTTAATAGTGAACCTGCACCTGATGCA 389922
QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564
Db 389921 CACTTTGAACTCAATCTGAACCAAGTTGATCAAGTTCAATACGACATTTATCAAAATGAA 389862
QY 565 ThrIleAlaProLysGlyArgGluLeuValVal-----PhePheSerLeuArgValAla 582
Db 389861 GAGCTAAACCAACTCTTGGACCGCTTTCAGATGATGATTTTTCAGAAACAACCACT 389802
QY 583 -----AsnMetAlaPheSerAsnAspLeu-PheAsnLys----- 593
Db 389801 GATCAAAACTATGTTTGTGATACCGCTTACCACGAGAGTAAACCAACCTGAATCAGTT 389742
QY 594 -----SerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln----- 607
Db 389741 GTTGACCAAGCTTCTTCAGATGATCATTTTGCACAAACAACCTGAATCAACTGATAGC 389682
QY 608 -----LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLys----- 621
Db 389681 TACAGCTTTGACAGTGATTTACCTCAACCAACCTTGACCAACCTTCTTTAGATGATCAT 389622
QY 622 ----GlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLys----- 638
Db 389621 GTTCAGTACAACTTTGATCACCATGAGAGCTCAACCACTGCTGCTGAAGAACCAATAAT 389562
QY 639 -----MetLysPheAlaLysSerVal-----ProTyrAsnLe 649
Db 389561 TATCAAGTTGGATTTGATCAAGTTCAAGCTAATCTTGATTAATAGAGGAATACACCA 389502
QY 649 uThrIleAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHi 669
Db 389501 -ACT---GCTGAAAAGAAGTAACACTACTGATTTTGAAGAATAAAGCCCAA----- 389454
QY 669 sLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
Db 389453 ----GTAGTTGATAGTTACCAATTTACCAATGAT---ACAGATCAACAAGACCAACAAC 389401
QY 689 sPheLeuAlaCysGlyGluPheAlaGlnCysValLys-----AsnGluArgThrGluGI 707
Db 389400 TTTTTCCTCTTCATTTGAAACTCAACCAAGATGAGCAGTTTGATCAAGTAATAAGCGA 389341
QY 707 uAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPr 727
Db 389340 AGTTAAGCATCAATTCAACTGAAATTAACCTAAG-----GAGCC 389302
QY 727 oglyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCy 747
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Db 389301 AGTTTGAAGAGTAGTTTTCATATAACAA----- 389274
QY 747 sArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAs 767
Db 389273 -----GATGTAGTTGAAACTAGTAACCTACACTAATAATTTACAGAAATTTGATAT 389224
QY 767 nGlnGlnAsnAsnLys-----ValIleSerLysArgAsnSer 779
Db 389223 TCAGTCTGATAATAAGATAACTATCATTACCAAAAAAGTTCA 389181
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Search completed: March 2, 2004, 00:54:49  
Job time : 892 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 14:40:11 ; Search time 775 Seconds  
(without alignments)

4368.792 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLETRRAIFVWFIFLQVQG.....NSELLTVEEENHODWEGN 757

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2.1/USPTC spool/US10007270/runat 25022004 164206 27185/app query.fasta\_1.967  
-DB=N\_Geneseq\_29Jan04 -QWT=fastap -SUFFIX=mg -MINWATCH=0.1 -LOOPEC=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_29Jan04.\*

1: geneseq1980s.\*  
2: geneseq1990s.\*  
3: geneseq2000s.\*  
4: geneseq2001as.\*  
5: geneseq2001bs.\*  
6: geneseq2002s.\*  
7: geneseq2003as.\*  
8: geneseq2003bs.\*  
9: geneseq2003cs.\*  
10: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	4073	98.9	3330	7 ADA14840	ADA14840 Human int
2	4073	98.9	3330	8 ACC57946	ACC57946 Human int
3	4039.5	98.1	3263	3 AAA46205	AAA46205 cDNA enco
4	4024.5	97.8	3261	7 ADA14866	ADA14866 Human CDN
5	4024.5	97.8	3261	8 ACC57960	ACC57960 Human int
6	3619	87.9	2887	7 ADA14842	ADA14842 Human int
7	3619	87.9	2887	8 ACC57947	ACC57947 Human int
8	3526.5	85.7	2966	3 AAA46328	AAA46328 Interphot

9	3323	80.7	2244	3 AAA46329	AAA46329 Interphot
10	3323	80.7	2244	7 ADA14844	ADA14844 Human int
11	3323	80.7	2244	8 ACC57948	ACC57948 Human int
12	2548.5	61.9	3668	7 ADA14847	ADA14847 Mouse int
13	2548.5	61.9	3668	8 ACC57950	ACC57950 Mouse int
14	2192	53.2	3206	3 AAA46309	AAA46309 cDNA enco
15	1342.5	32.6	1726	7 ADA14849	ADA14849 Mouse int
16	1342.5	32.6	1726	8 ACC57951	ACC57951 Mouse int
17	929.5	22.6	1321	7 ADA14851	ADA14851 Mouse int
18	929.5	22.6	1321	8 ACC57952	ACC57952 Mouse int
19	927	22.5	4165	3 AAA46206	AAA46206 cDNA enco
20	927	22.5	4166	7 ADA14855	ADA14855 Human int
21	927	22.5	4166	8 ACC57954	ACC57954 Human int
22	885	21.5	555	3 AAA46204	AAA46204 cDNA enco
23	885	21.5	555	7 ADA14853	ADA14853 Monkey in
24	885	21.5	555	8 ACC57953	ACC57953 Monkey in
25	846.5	20.6	2364	7 ADA14857	ADA14857 Human int
26	846.5	20.6	2364	8 ACC57955	ACC57955 Human int
27	841	20.4	4204	3 AAA46310	AAA46310 cDNA enco
28	841	20.4	4204	7 ADA14862	ADA14862 Mouse int
29	841	20.4	4204	8 ACC57958	ACC57958 Mouse int
30	241	5.9	1094	3 AAA46321	AAA46321 Exon 13 o
31	192.5	4.7	1817	3 AAA46320	AAA46320 Exon 12 o
32	189.5	4.6	4139	6 ABL67071	ABL67071 Thyroid c
33	189.5	4.6	4139	6 ABL67544	ABL67544 Thyroid c
34	189.5	4.6	4139	6 ABL68884	ABL68884 Kidney ca
35	189.5	4.6	4139	6 ABK09797	ABK09797 Human ova
36	189.5	4.6	4139	6 ABN95623	ABN95623 Gene #212
37	189.5	4.6	4139	7 ACC50234	ACC50234 Breast ca
38	189.5	4.6	4139	7 ACF12907	ACF12907 Human cer
39	188.5	4.6	1572	5 AAS00585	AAS00585 Human MUC
40	188.5	4.6	1721	6 ABS76475	ABS76475 cDNA enco
41	188.5	4.6	1721	6 ABL68032	ABL68032 Ovary can
42	188.5	4.6	1721	6 ABK09743	ABK09743 Human ova
43	188.5	4.6	1721	6 ABV94067	ABV94067 Breast ca
44	188.5	4.6	1721	7 ADA50566	ADA50566 Mucin 1 (
45	188.5	4.6	1721	7 ACF12906	ACF12906 Human cer

#### ALIGNMENTS

RESULT 1

ADA14840

ID ADA14840 standard; cDNA; 3330 BP.

XX ADA14840;

XX AC

XX DT

XX 06-NOV-2003 (first entry)

XX Human interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.

XX ss; gene; human; IPMC 150 isoform A; gene therapy;

XX interphotoreceptor matrix component; IPMC; ocular disorder;

XX macular degeneration; photoreceptor death; retinal detachment.

XX OS Homo sapiens.

XX FH Key

XX CDS

XX Location/Qualifiers

XX 131..2586

XX /tag= b

XX /product= "IPMC 150 isoform A"

XX /transl\_except= (pos:689..756,aa:Thr-Asp)

XX 131..150

XX /tag= a

XX /label= Signal\_sequence

XX 191..2583

XX /tag= c

XX /label= Mature\_IPMC\_150\_isoform\_A

XX 692..753

XX /tag= d

XX /note= "This region could represent intronic sequence not removed from the cDNA sequence"

XX

XX



PN US2002160954-A1.  
 XX 31-OCT-2002.  
 PD 08-NOV-2001; 2001US-00007270.  
 PF 29-OCT-1998; 98US-00183972.  
 PP 29-OCT-1999; 99US-00430195.  
 PR (IOWA ) UNIV IOWA RES FOUND.  
 XX Hageman GS, Kuehn MH;  
 XX WPI: 2003-238235/23.  
 XX P-PSDB; ADA14841.  
 DR  
 XX New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX  
 PS Claim 3; Page 29-30; 76pp; English.  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform A.  
 XX  
 SQ Sequence 3330 BP; 1069 A; 737 C; 574 G; 850 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0 Length: 3330  
 Score: 4073.00 Matches: 796  
 Percent Similarity: 97.31% Conservative: 0  
 Best Local Similarity: 97.31% Mismatches: 1  
 Query Match: 98.93% Indels: 22  
 DB: 7 Gaps: 1

US-10-007-270-2 (1-797) x ADA14840 (1-3330)

QY	1	MetTyrLeuGluThrArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly	20
DB	131	ATGTATTGGAACTAGAGAGACTATTTTGGTTTGGATTCTTCTCAAGTTCAGGA	190
QY	21	ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro	40
DB	191	ACCAAGATATCTCCATTAAACATATACCATTTCTGAAACTAAGACATAGACAATCCCCCA	250
QY	41	ArgAsnGluThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile	60
DB	251	AGAAATGAACAACTGAAAGTACTGAAATAATGTACAAAATGTCACATATAGAGCAATA	310
QY	61	PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal	80
DB	311	TTTCGATTTCGAAAGCATCGAACAAAGATCCGCATTTTCCCAACGGGGTAAAGTC	370
QY	81	CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg	100
DB	371	TGTCACAGGAATCCCATGAACAGATTTTAGACAGTCTTCAAGCTATTATAGATTGAGA	430
QY	101	ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgileProAspThr	120
DB	431	GTGTGTCCAGGAACAGATATGGGAGCATATCGGATCTTTCTCGATCGCATCCCTCACACA	490
QY	121	GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle	140
DB	491	GGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATT	550

QY	141	GlyLysAsnPheSerAsnSerGlnGlnIleHisLeuAspLeuGlnGlnArgIleLysGln	160
DB	551	GGAAATAAACTTCAGCAATTCAGGAGCACCTGGATCTTCTCCAGCAGAGATAAAGAG	610
QY	161	ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyLysProGly	180
DB	611	AGNAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAGACATTGGGAGAGCTGCT	670
QY	181	GluThrIleValIleSerThr	187
DB	671	GAACCAATTGTCTATTTCAC-AGCAATCTACATTTCAAAGACTTGGGCAGTATTCTAAGA	729
QY	188	-----AspValAlaAsnValSerLeuGlyProPheProLeu	199
DB	730	AAACCTCAGAGAGCAAAATTCAGATGTTGCCAAGCTCTCACTTGGGCTTTCCTCTC	789
QY	200	ThrProAspAspThrLeuAsnGlnIleLeuAspAsnThrLeuAsnAspThrLysMet	219
DB	790	ACTCTGATGACACCTCCTCAATGAATTTCTGATAATACACTCAACGACACCAAGATG	849
QY	220	ProThrThrGluArgGluThrGluPheAlaValLeuGluGluArgValGluLeuSer	239
DB	850	CCTACCAACAGAGAGAGAAACAGATTCGCTGTGTTGGAGGAGCAGGGTGGAGCTCAGC	309
QY	240	ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr	259
DB	910	GTCTCTCTGTAAACCAGAAAGTTCAAGGCAGAGCTCGCTGACTCCAGTCCCACATATTAC	969
QY	260	GlnGluLeuAlaGlyLysSerGlnIleGlnMetGlnLysIlePheLysLysLeuProGly	279
DB	970	CAGGACTAGCAGGAAGTCCCAACTTCAGATTCAGAAAGATATTTAAGAAATTCACAGA	1029
QY	280	PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer	299
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QY	300	ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla	319
DB	1090	ACAGAGATGCACATTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCA	1149
QY	320	SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr	339
DB	1150	AGTGACCTCTCTCTTTTGTATCCCAAAAATTTGAAGTGAAGAGTCTATCATGGAACC	1209
QY	340	MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle	359
DB	1210	ATGGAGGAGACAAAGCAACCCAGAAATCTATCTCACAGCTACAGACCTCAAAAGGCTGATC	1269
QY	360	SerLysAlaLeuGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu	379
DB	1270	AGCAAGCAGCTAGAGGAAGAACAACTTTGGATGTGGGACCAATTCAGTTCCTGATGAA	1329
QY	380	IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe	399
DB	1330	ATTGTGGATCACTGCCAGCTTTGGTCTGTGACCCCAATCAGAGCTGCCCATCTTTT	1389
QY	400	AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu	419
DB	1390	GCTGTTATACAGAGATGCTACTTTGAGTCCAGAACTCTCTCTCTTGAACCCAGCTT	1449
QY	420	GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrSerProProAlaMet	439
DB	1450	GAGCAGTGGACGAGCAGAGCATGTCTACCTGACACTTCTGGTCTCCACCTGCTATG	1509
QY	440	AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu	459
DB	1510	GCCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTCG	1569
QY	460	ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu	479
DB	1570	ACTGATCAAGGCACACAGATACAAATGGCCACTGACCAGACAAATGCTAGTACCAGGCTC	1629

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1750	GAT	CAA	ATG	GAT	CTG	T	CGA	CTCT	CT	CGCC	CAAT	CTG	AGG	TAC	GAG	AGCT	TC	AGC	GAAT	1809	
540	Val	Ser	Val	Pro	Asp	His	Phe	Leu	Glu	Asp	Thr	Thr	Pro	Val	Ser	Ala	Leu	Gln	Tyr	Ile	559
1810	GT	TTCT	GTCC	AGAT	CA	TTTCT	TGG	AGG	ATAC	CACT	CTCT	CTCT	CAG	CTT	TAC	AGT	ATAT	C		1869	
560	Thr	Thr	Ser	Ser	Met	Thr	Ile	Ala	Pro	Leu	Gly	Arg	Glu	Leu	Val	Val	Phe	Phe	Ser	Leu	579
1870	ACC	ACT	AGT	TTCT	AT	GAC	CAAT	TG	CCCC	CA	AGG	CGC	AG	AGCT	TGT	AGT	TGT	TTCT	TTCT	1929	
580	Arg	Val	Ala	Asn	Met	Ala	Phe	Ser	Asn	Asp	Leu	Phe	Asn	Leu	Ser	Ser	Leu	Glu	Tyr	Arg	599
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1990	GCT	CTG	GAG	CAACAA	TTT	CA	CAC	AGCT	GCT	GGT	CCAT	TAT	CT	AC	GAT	CCAAT	CTT	CAG	GA	2049	
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640	Lys	Phe	Ala	Lys	Ser	Val	Pro	Tyr	Asn	Leu	Thr	Lys	Ala	Val	Ile	Gly	Val	Leu	Glu	Asp	659
2110	AAG	TTT	GCT	TAAG	CT	TG	TG	CCG	TATA	CACT	CA	CA	AGG	CTG	CA	CGG	GCT	TTG	GAG	AT	2169
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680	Glu	Pro	Ala	Asp	Gln	Ala	Asp	Pro	Cys	Lys	Phe	Leu	Ala	Cys	Gly	Glu	Phe	Ala	Gln	Cys	699
2230	GA	ACC	AGCT	GTAT	CA	AGC	AGAT	CCCT	CG	CAAGT	CTCT	GG	CCCT	CG	CGG	CAAT	TTG	CCCAAT	TGT	2289	
700	Val	Lys	Asn	Glu	Arg	Thr	Glu	Glu	Ala	Gly	Cys	Arg	Cys	Lys	Pro	Gly	Tyr	Asp	Ser	Gln	719
2290	GTA	AGAAC	CAAC	CGG	ACT	GT	AG	GAAG	CGG	AGT	TGCT	GT	CAAA	CCAG	GAT	ATG	CA	CC	CCAG	2349	
720	Gly	Ser	Leu	Asp	Gly	Leu	Glu	Pro	Arg	Lys	Cys	Gly	Pro	Gly	Thr	Lys	Gly	Cys	Glu	Val	739
2350	GGG	AGCCT	GTG	CGGT	CT	GG	AAC	CAG	CGCT	CTGT	GG	CCCT	TGG	CA	AAAG	GAAT	TGG	AGG	TCT	2409	
740	Leu	Gln	Gly	Lys	Gly	Ala	Pro	Cys	Arg	Leu	Pro	Asp	His	Ser	Glu	Asn	Gln	Ala	Tyr	Lys	759
2410	CTC	CAG	GGAA	AGG	AGCT	CT	CA	TG	CGG	TTT	GCC	AGAT	CAC								

XX	Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX	receptor; ophthalmological; gene therapy; gene; ss.
XX	Homo sapiens.
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XX	DR
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FT /product= "Variant IPMC 150 isoform A"  
XX US2002160954-A1.  
PD 31-OCT-2002.  
XX 08-NOV-2001; 2001US-00007270.  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX WPI; 2003-238235/23.  
XX P-PSDB; ADA14867.  
XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX Claim 3; Page 63-66; 76pp; English.  
XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)

CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding  
 CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
 XX

50 Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.: 4,32e-316 Length: 3261  
 Score: 4024.50 Matches: 793  
 Percent Similarity: 99.62% Conservations: 1  
 Best Local Similarity: 99.50% Mismatches: 3  
 Query Match: 97.75% Indels: 3  
 DB: 7 Gaps: 0

US-10-007-270-2 (1-797) x ADA14866 (1-3261)

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 Db 128 ATGTATTGGAACTAGAGAGCTATTATTTTGTGTTTGGATTTTCTCCAAAGTCAAGGA 187  
 Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 Db 188 ACTAAGATATCTCCATTACATATACCAATCTGAAGACTTAAGACATAGACATCCCCA 247  
 Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 Db 248 AGAAATGAACCACTGAAGTACTGAAAAATGTACAAAATGTCAACTATGAGACGAATA 307  
 Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 308 TTCGATTTGGCAAGCATCGACAAAAGATCCGCATTTTCCACGGGGGTTAAGTC 367  
 Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTrpArgLeuArg 100  
 Db 368 TGTCACAGGAATCCATGAAACAGATTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 427  
 Qy 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 428 GTGTGTGAGGAGCAGTATGGGAGCATATCGGATCTTCTGGATCGCATCCCTTGACACA 487  
 Qy 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 488 GGGGAATATCAGGACTGGGTGACATCTGCCAGCAGGAGACCTTCTGCCCTTTTGACATT 547  
 Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160  
 Db 548 GGAAAAAACTTCAGCAATTCAGAGACCTGGATCTTCCAGCAGAGAAATAAACAG 607  
 Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 Db 608 AGAAGTTCCCTGACAGAAAGATGAATATCTGCAGAGAGACATTTGGAGAGCCTGGT 667  
 Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 668 GAAACCATTTGTCAATTCACAGATGTTGCCAACGCTCTCACTTGGGCTTTCCCTCTCACT 727  
 Qy 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 Db 728 CCTGATGACACCCCTCTCAATGAATTTCTCGATTAATACATCTCAACGACACCAAGATGCCT 787  
 Qy 221 ThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerVal 240  
 Db 788 ACAACAGAAAGAGAAACAGAAATTCGTGTGTGTGGAGGAGCAGAGGGTGGAGCTCAGCGTC 847  
 Qy 241 SerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260  
 Db 848 TCTCTGGTAAACCAAGAGTTCAGAGCAGAGCTCGCTCACTCCCACTCCCATATTACCAG 907  
 Qy 261 GluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280

Db 908 GAGCTAGCAGGAAAGTCCCACTTCAGATGCAGAAAGATATTAAAGAACTTCCAGGATTTC 967  
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 Db 968 AAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACA 1027  
 Qy 301 GluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProLaser 320  
 Db 1028 GAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGT 1087  
 Qy 321 AspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMet 340  
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 Qy 341 GluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360  
 Db 1148 GAGGAGGACAAAGCAACCAAGATCTATCTCAGCAGTACAGACCTCAAAAGCGTGTATCAGC 1207  
 Qy 361 LysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
 Db 1208 AAAGCACTAGAGGAAGAAACATCTTTGGATGTGGGACAAATTCAGTTCATGTGAATTT 1267  
 Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 Db 1268 GCTGGATCACTGCCAGCCTTTGGTCTGACACCAATCAGAGCTGCCACATCTTTTGTCT 1327  
 Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeuGlu 420  
 Db 1328 GTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTGTGTAACCCAGCTTGAG 1387  
 Qy 421 ThrValAspGlyValAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMetAla 440  
 Db 1388 ACAGTGGACGGCAGCAGCATGGTCTACCTGACACTTCTGTGTCTCCACCTGTATGCC 1447  
 Qy 441 SerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeuThr 460  
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 Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500  
 Db 1568 ATCCCCCAGCAGTATTCTGCAATCAGCAACTGGCTCTGGAAATTTCACTCACTCACT 1627  
 Qy 501 AlaSerSerAspAspSerArgSerSerAlaGlyGluAspMetValArgHisLeuAsp 520  
 Db 1628 GCATCTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGGTCAGACACCTAGAT 1687  
 Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540  
 Db 1688 GAAATGGATCTGTCTGACACTCTGCCCACTCTGAGGTACCAAGCTCAGCGAATATGTT 1747  
 Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
 Db 1748 TCTGTCCAGCATCACTTCTTGAGGATACCACTCTCTGCTCAGCTTTACAGTATATCACC 1807  
 Qy 561 ThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeuArg 580  
 Db 1808 ACTAGTCTTATGACCATTTGCCCCCAAGGGCGAGAGCTGGTAGTGTCTTCTCAGTCTCGT 1867  
 Qy 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
 Db 1868 GTTGTAAACATGGCTTCTCCAACGACCTGTTCACAAAGAGCTCTCTGGAGTACCGAGCT 1927  
 Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
 Db 1928 CTGGAGCAACCAATTCACAGCTGTGTGTTCCATATCTACCATCCAATCTTACAGGATTT 1987  
 Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640

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Db 1988 AAGCAACTGTAATACCTTAACTTCAGAAACGGAGTGTGATTGTGAATAGCAAAATGAAG 2047
QY 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660
Db 2048 TTTGCTAAGTGTGTCCCTATAAAGCTTCAACCAAGGCTGTGCACGGGGTCTTTGGAGATTTT 2107
QY 661 ArgSerAlaAlaGlnGlnLeuHisLeuGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 680
Db 2108 CTTTCTGTGTGAGCCCAACACTCCACTGGAATAGACACTTCTCTCAACATTGAA 2167
QY 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700
Db 2168 CCAGCTGTATCAAGCAGATCCCTGCAAGTTCCTGGCTGGCGGAATTTGCCAATGTGTA 2227
QY 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720
Db 2228 AAGAACGAAACGACTGAGAACGGAGTGTCTGCTGCAACAGGATATGACAGCCAGGG 2287
QY 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740
Db 2288 AGCCTGGAGCGGTCTGGAACCAAGGCTCTGTGG-CCTGGCACAAGGAATGCGAGTCTCTC 2346
QY 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760
Db 2347 CAGGGAAGAGGAGCTCCATGGG--GTTCCAGATCACTGGAATCAAGCATACAAAAC 2404
QY 761 SerValLysLysPheGlnAsnGlnGlnAsnLysValLysSerLysArgAsnSerGlu 780
Db 2405 AGTGTTAA-AGTTTCCAAATCAACAAATAACAAGGTAAATCAGTAAAGAAATTCGTAA 2463
QY 781 LeuLeuThrValGluTyrGluGluPheAsnHisGlnAspThrGluGlyAsn 797
Db 2464 TTACTGACCGTAGAATATCAAGAAATTTAACCATCAAGATTGGGAAGGAAAT 2514
RESULT 5
ID ACC57960 standard; cDNA; 3261 BP.
XX AC ACC57960;
XX DT 11-AUG-2003 (first entry)
XX DE Human interphotoreceptor matrix IPM 150, isoform A variant, cDNA.
XX KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX KW receptor; ophthalmological; gene therapy; gene; ss.
XX OS Homo sapiens.
XX FH Key
XX CDS Location/Qualifiers
XX FT 128..2443
XX FT /*tag= a
XX FT /product= "IPM 150"
XX PN WO2003039346-A2.
XX XX
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036090.
XX PR 08-NOV-2001; 2001US-00077270.
XX XX (IOWA ) UNIV IOWA RES FOUND.
XX PA
XX XX Hageman GS, Kuehn MH;
XX XX WPI; 2003-441440/41.
XX DR P-P8DB; ABR42354.
XX XX
XX PT New interphotoreceptor matrix proteins and polynucleotides, useful for
XX PT treating or preventing photoreceptor death or retinal detachment, or for
XX PT treating ocular disorders.
XX XX
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PS Claim 1; Page 91-94; 105pp; English.
XX The present sequence is that of cDNA encoding a variant of isoform A of
CC novel human interphotoreceptor matrix 150 (IPM 150), a member of the
CC newly identified interphotoreceptor matrix component (IPMC) gene family.
CC The cDNA was isolated from a human retinal cDNA library. The IPM 150 gene
CC is located on chromosome 6q13-q15, a region that also contains loci for
CC progressive bifocal chorioretinal atrophy, autosomal dominant Stargardt's
CC like macular dystrophy, North Carolina macular dystrophy and Salla
CC disease. Members of the IPMC gene family have been identified in humans,
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2 IPMG2). The
CC subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC antibodies that specifically bind the polypeptides, and vectors
CC comprising the polynucleotides. A claimed method of treating or
CC preventing photoreceptor death or retinal detachment involves
CC administering an IPMC polynucleotide, polypeptide or antibody. Also
CC claimed is a method for identifying a compound capable of modulating IPMC
CC gene expression
XX XX
SQ Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 4,328-316 Length: 3261
Score: 4024.50 Matches: 793
Percent Similarity: 99.62% Conservative: 1
Best Local Similarity: 99.50% Mismatches: 3
Query Match: 97.75% Indels: 3
DB: Gaps: 0

US-10-007-270-2 (1-797) x ACC57960 (1-3261)
QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
Db 128 ATGTATTTCGAAACTAGAAAGACTATTTTGTGTTTTCGATTTTCTCCAAAGTTCAAGA 187
QY 21 ThrLysAspLysSerIleAsnIleTyrHisSerGluThrLysAspLysAspLysMetSer 40
Db 188 ACTAAAGATATCTCCATTTAACTATACCATTTCTGAACTAAAGACATAGACAAATCCCCA 247
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgIle 60
Db 248 AGAATGAAACCAACTGAAAGTACTGAAAAAATGTACAAAATGTCAAAATATGACATATGAGACGAATA 307
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
Db 308 TTCGATTTCGCAAGCATCGAAACAAAAGATCCGATTTTCCCAACGGGGGTTAAAGTC 367
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db 368 TGTCACACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 427
QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db 428 GTGTGTGAGAAAGCAGATATGGGAAGCATATCGGATCTTTCTCGATCGCATCCCTGACACA 487
QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140
Db 488 GGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTCGACATT 547
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160
Db 548 GGAATAAACTTCAGCAATTTCCAGGAGCACCTTGGATCTTCTCCAGCAGAGAATAAAACAG 607
QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
Db 608 AGAAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAAACATTTGGAGAGGCTGTGT 667
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db 668 GAATCCATTGTCTATTTCAACAGATGTTGCCAAGCTTCTACTTGGGCTTTCCTCTCACT 727
QY 201 ProAspAspThrLeuLeuAsnGlnIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
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Db 728 CCTGATGACCCCTCCTCAATGAAATTCGATAATACCTCAACGACACCAAGATGCCT 787  
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Qy 241 SerLeuValAenGlnLysPheGlyAlaGluLeuAlaAspSerGlnSerProTyrGln 260  
Db TCTCTGGTAAACCAAG 907  
Qy 261 GluLeuAlaGlyLysSerGlnGluMetGlnLysIlePheLysLysLeuProGlyPhe 280  
Db GAGTAGCAG 967  
Qy 281 LysLysIleHsValLeuGlyPheArgProLysLysGluLysAspGlySerSerThr 300  
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Qy 301 GluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSer 320  
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Qy 341 GluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360  
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Qy 361 LysAlaLeuGluGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
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Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeuGlu 420  
Db GTTATACAG 1387  
Qy 421 ThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMetAla 440  
Db ACAGTGGACGAG 1447  
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Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500  
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Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540  
Db GAAATGGATCTGCTGACACTCTGCCCATCTGAGGTACAGAGCTCAGCGAATATGTT 1747  
Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
Db TCTGTCCAGATCATTTCTCGAGAGATACCACTCTCTGCTCAGCTTTACAGTATATCACC 1807  
Qy 561 ThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeuArg 580

Db 1808 ACTAGTCTATGACCAATTCGCCCCAGGCGGAGAGCTGGTAGTCTTCTCAGTCTGCGT 1867  
Qy 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
Db 1868 GTTGCTAAACATGCGCTTCTCCAAACGACCTGTCAACAAGAGCTCTCTGGAGTACCGAGCT 1927  
Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
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Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
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Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
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Qy 661 ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
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Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720  
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Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740  
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Qy 761 SerValLysLysPheGlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsnSerGlu 780  
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Qy 781 LeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTrpGluGlyAsn 797  
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RESULT 6  
ADA14842 standard; cDNA; 2887 BP.  
ID ADA14842 (first entry)  
AC ADA14842;  
XX 06-NOV-2003  
DT Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.  
DE ss; gene, human; IPMC 150 isoform B; gene therapy;  
XX interphotoreceptor matrix component; IPMC; ocular disorder;  
KW macular degeneration; photoreceptor death; retinal detachment.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 5..2143  
CDS /tag= a  
FT /partial  
FT /product= "IPMC 150 isoform B"  
FT /note= "No start codon given. Encodes residues 8-719 of  
FT {seqid:4}"  
PN US2002160954-A1.  
PD 31-OCT-2002.



XX PF 08-NOV-2001; 2001US-00007270.  
 XX PR 29-OCT-1998; 98US-00183972.  
 XX PR 29-OCT-1999; 99US-00430195.  
 XX PA (IOWA ) UNIV IOWA RES FOUND.  
 XX PI Hagaman GS, Kuehn MH;  
 XX WPI; 2003-238235/23.  
 XX DR P-PSDB; ADA14843.  
 XX PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX PS Claim 3; Page 33-34; 76pp; English.  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform B.  
 XX SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: Length: 2887  
 Score: 3619.00 Matches: 711  
 Percent Similarity: 90.00% Conservative: 0  
 Best Local Similarity: 90.00% Mismatches: 1  
 Query Match: 87.90% Indels: 78  
 DB: 7 Gaps: 1  
 US-10-007-270-2 (1-797) x ADA14842 (1-2887)  
 QY 8 AlaIlePheValPheThrIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27  
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 QY 28 IleTyrHisSerGluThrLysAspIleAsnProArgAsnGluThrThrGluSer 47  
 DB 49 ----- 49  
 QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67  
 DB 49 ----- 49  
 QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87  
 DB 49 ----- 49  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuA-gValCysGlnGluAlaValTrp 107  
 DB 50 -----GTGTGTCAGGAAGCAGTATGG 70  
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 DB 71 GAAGCATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGACTGGGTC 130  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
 DB 131 AGCATCTGCAGCAGAGACCTTCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTC 190  
 QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167

DB 191 CAGGACACCTGGATCTTCTCCAGCAGAGATAAAACAGAGAAGTTTCCCTCAGACAAAA 250  
 QY 168 AspGluIleSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
 DB 251 GATGAAATATCTGCAGAGAAGACATTTGGGAGAGCTGGTGAACCACTGTCTATTTCAACA 310  
 QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
 DB 311 GATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTCTCACTCTGTATGACACCCCTCCTCAAT 370  
 QY 208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227  
 DB 371 GAAATTTCTGATAATACACTCAACGACACCAAGATGCTTACACAGAAAGAGAGAAACAGAA 430  
 QY 228 PheAlaValIleGluGlnGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
 DB 431 TTCCCTGTGTTGGAGGAGCAGAGGGTGGAGCTCAGGCTCTCTCTGTTAAACACAGAGTTT 490  
 QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267  
 DB 491 AAGGCAGAGCTCGCTGACTCCCGATCCCATATATACAGAGCTAGCAGAAAGTCCCAA 550  
 QY 268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
 DB 551 CTTTCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAAAAAATCCATGTGTAGGA 610  
 QY 288 PheArgProLysLysGlyLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
 DB 611 TTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATC 670  
 QY 308 PheLysArgHisSerAlaGluLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
 DB 671 TTTAAGAGACACAGTGCAGAAACAAAGCCCTGCAAGTGACTCTCTGCTTTTGATTC 730  
 QY 328 AsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347  
 DB 731 AACAAATTTGAAGTGAAGAGTCTATCATGGAACCATCGAGAGGACCAAGCAACAGAA 790  
 QY 348 IleTyrLeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlnGluGln 367  
 DB 791 ATCTATCTCAGACTACAGACCTCAAAAGCTGATCAGCAAAAGCCTAGAGGAAGAACAA 850  
 QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
 DB 851 TCCTTGGATGAGGAGCAATTCAGTCACTGATGAATTCCTGGATCATCTGCAGGCTTT 910  
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 DB 911 GGTCCTGACACCAATCAGAGCTGCCACATCTTTTGTCTGTATATAACAGAGGATGCTACT 970  
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 QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
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QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
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QY 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
Db 1391 GAGGATACATCTCTGTCTCAGCTTACAGTATATACCATAGTTCATGACCATTTGCC 1450
QY 568 ProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db 1451 CCCAAGGGCCGAGAGCTGGTAGTGTCTTCACTAGCTGCGTGTGCTAAACATGGCCCTTCTCC 1510
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGln 607
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QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
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Db 1691 AACCTCACCAAGGCTGTGCAGGGGTCTTGGAGATTTTCGTTCTGTGAGGCCCAACAA 1750
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
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QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
Db 1811 TGCAGATTCTCGGGCTGCGGGAATTTGCCCAATGTGTAAGAACGACGACTGAGGAA 1870
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
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QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db 1931 GGCCTCTGTGCCCTGGCACAAAGGAATCGGAGTCTCTCCAGGGAAGGGAGCTCCATGC 1990
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767
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QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
Db 2051 CAACAAAATAACAAGGTAAATCAGTAAAGAAATTTCTGAATTAATCTGACCGTAGAATATGAA 2110
QY 788 GluPheAsnHisGlnAspTyrGluCysAsn 797
Db 2111 GAATTTAAACCATCAAGATTGGGAAGGAAT 2140
RESULT 7
ACCS57947
ID ACC57947 standard; cDNA; 2887 BP.
XX ACC57947;
AC ACC57947;
XX
XX 11-AUG-2003 (first entry)
XX Human interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX
XX Human interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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CDS
FT 2. .2143
FT /*tag= a
FT /product= "IPM 150"
FT /partial
FT /note= "No start codon"
XX
XX WO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-441440/41.
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
XX Claim 1; Page 78-79; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform B of novel human
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 6q13-q15, a region that also contains loci for
XX progressive bifocal chorioretinal atrophy, autosomal dominant Stargardt's
XX -like macular dystrophy, North Carolina macular dystrophy and Salla
XX disease. Members of the IPMC gene family have been identified in humans,
XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
XX antibodies that specifically bind the polypeptides, and vectors or
XX comprising the polynucleotides. A claimed method of treating or
XX preventing photoreceptor death or retinal detachment involves
XX administering an IPMC polynucleotide, polypeptide or antibody. Also
XX claimed is a method for identifying a compound capable of modulating IPMC
XX gene expression
XX
XX Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	2,788-283	Length:	2887
Score:	3619.00	Matches:	711
Percent Similarity:	90.00%	Conservative:	0
Best Local Similarity:	90.00%	Mismatches:	1
Query Match:	87.90%	Indels:	78
DB:	8	Gaps:	1

US-10-007-270-2 (1-797) x ACC57947 (1-2887)

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QY 8 AlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27
Db 5 GCTATTTTGTGTTTGTGATTTTCTCCAAGTCAAGGAACCAAA----- 49
QY 28 IleTyrHisSerGluThrLysAspIleAspAsnProProArgAsnGluThrThrGluSer 47
Db 49 ----- 49
QY 48 ThrGluLysMetTyrLysMetSerThrMetArgIlePheAspLeuAlaLysHisArg 67
Db 49 ----- 49
QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87
Db 49 ----- 49
QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107

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50 -----GTGTCTCAGGAAGCAGATGCG 70  
108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrVal 127  
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128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
131 AGCATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATTTGGAAAAAACTTCAGCAATTC 190  
148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
191 CAGGAGCACCTTGGATCTTCTCCAGCAGAGATAAAACAGAGAGTTTCCCTGCAGAGAAA 250  
168 AspGluIleSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
251 GATGAATATCTGAGAGAAACATTTGGAGAGCTTGGTGAACCATTTGATTTCAACA 310  
188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspThrLeuLeuAsn 207  
311 GATGTTCACACGCTCACTTGGGCTTTCCCTCTCACTCTGATGACACCTTCTCAAT 370  
208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227  
371 GAAATTTCTCGATAATACACTCAACGACACCAAGATGCTCAACAGAGAAAGAGAAACAGAA 430  
228 PheAlaValLeuGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
431 TTCGTGTGTGGAGGACAGAGGTGGAGCTCAGCGCTCTCTGTGTAAACACAGAGATTTC 490  
248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267  
491 AAGGCAGAGCTCGTGTGCTCCAGTCCCATATTAACAGGAGCTAGCAGGAAAGTCCCAA 550  
268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
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288 PheArgProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIle 307  
611 TTTAGACCAAGAAAGAAAGATGGCTCAAGTCCACAGAGATGCAACTTACGCCATC 670  
308 PheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
671 TTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTACCTCTCTGTTGATTC 730  
328 AsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347  
731 AACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGACCAAGCAACAGAA 790  
348 IleTyrLeuThrAlaThrAspLeuLysArgIleLysSerLysAlaLeuGluGluGln 367  
791 ATCTATCTCACAGCTACAGACCTCAAAAGGCTGTATCAGCAAGCAGCTAGAGGAAAGCAA 850  
368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
851 TCTTTGGATGTGGGACAAATTCAGTTCACTGATGAATTTGGTCACTCCAGCCTTT 910  
388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
911 GGTCTCTGACACCAATCAGAGCTGCCACATCTTTTGTCTTATATAACAGAGGATGCTACT 970  
408 LeuSerProGluLeuProProValGluProGlnLeuThrValAspGlyValaGluHis 427  
971 TTGAGTCCAGAACTTCTCTCTTTGAACCCAGCTTGAGACAGTGGAGCGGACGAGCAT 1030  
428 GlyLeuProAspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAla 447  
1031 GGTCTACCTGACATCTTGGTCTCCACTGCTATGGGCTCTTACCTCTCTGTCAGAGCT 1090  
448 ProProPhePheValaSerSerIlePheSerLeuThrAspGlnGlyThrAspThr 467  
1091 CCACCTTTCTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGACCCACAGATACA 1150

QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
Db 1151 ATGGCCATGTACAGACAATGCTAGTACCAGGCTCACCATCCCACAGTGATATTCT 1210  
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArg 507  
Db 1211 GCATATCGCAACTGGCTCTGGGAATTTCAATCCACTGCATCTTCAGATGACAGCCGA 1270  
QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
Db 1271 TCAAGTCAGGTGGGGAAGATATGTCAGACACTAGATGAATGAATGATCTCTTGCACT 1330  
QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 1331 CTGCCCCCATCTGAGGTACCGGCTCAGCGAATACGTTTCTGCCAGATCAITTTCTTG 1390  
QY 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567  
Db 1391 GAGGATACCACTCCTGCTCTCAGCTTTACAGTATATCACCATAGTTCTATGACCAATGCC 1450  
QY 568 ProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
Db 1451 CCCAAGGCCGAGAGCTGTAGTGTCTTCAGTCTCGGTGCTGTAACTGSCCTTCTCC 1510  
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
Db 1511 AACGACCTGTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAG 1570  
QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627  
Db 1571 CTGCTGTGTTCCATATCTAGATCCAAATCTTACAGATTTAAGCACTTGAATATCTTAAC 1630  
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
Db 1631 TTCAGAAACCGGAGTGTGATTGTGAATAGCAAAATGAAGTTTGTCTGCTGCGGTAT 1690  
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667  
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QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
Db 1751 CTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACCAAGCTGATCAAGCAGATCCC 1810  
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707  
Db 1811 TGCAGATTCTCTGCGCTGCGCGAATTTGCCAATGTGTAAAGAACGAACGAGCTGAGGAA 1870  
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727  
Db 1871 GCGGAGTGTCTGTCMAACAGGATATGACAGCCAGGGGAGCTGAGCGGTCTGGAACCA 1930  
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747  
Db 1931 GGCCTCTGTGGCCCTGGCACAAGGAATGCGAGTCTCTCCAGGGAAAGGAGCTCATGCG 1990  
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767  
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RESULT 8

AAA46328

ID AAA46328 standard; DNA; 2966 BP.

XX

AC

AAA46328;

XX

04-SEP-2000 (first entry)

XX

Interphotoreceptor matrix proteoglycan (IPM150) splice variant.

DE

XX

Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200; chromosome 6q13-q15; ocular disease; retinal detachment; choriorretinal degeneration; retinal degeneration; cone degeneration; age related macular degeneration; photoreceptor degeneration; retinal pigment epithelium degeneration; mucopolysaccharidosis; rod- cone dystrophy; cone-rod dystrophy; ss.

XX

Homo sapiens.

OS

WO200026367-A2.

XX

11-MAY-2000.

XX

29-OCT-1999; 99WO-US025440.

XX

29-OCT-1998; 98US-00183972.

PR

(IOWA ) UNIV IOWA RES FOUND.

XX

Hageman GS, Kuehn MH;

PI

WPI; 2000-365516/31.

XX

Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for preventing, diagnosing and treating ocular disorders such as retinal detachment and choriorretinal degeneration.

DR

Claim 3; Fig 18; 183pp; English.

XX

The present sequence represents a splice variant of an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The sequence is missing exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15, between markers CHLC.GATALLF10 and D6S284. The IPM proteins may be used to supplement a patient's own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, choriorretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, RP (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

CC

Sequence 2966 BP; 918 A; 587 C; 524 G; 737 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:	9.11e-276	Length:	2966
Score:	3526.50	Matches:	707
Percent Similarity:	89.62%	Conservative:	1
Best Local Similarity:	89.49%	Mismatches:	4
Query Match:	85.66%	Indels:	81
DB:	3	Gaps:	1

US-10-007-270-2 (1-797) x AAA46328 (1-2966)

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8 AlaIlePheValPheThrIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27

DB

5 CCTATTTTGTGTTTGGATTTTCTCCAGTTCAGAACCAAA-----49

QY

28 IleTyrHisSerGluThrLysAspIleAspAsnProProArgAsnGluThrThrGluSer 47

DB

49 -----49

48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67

QY

49 -----49

DB

68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87

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49 -----49

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QY

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DB

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QY

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DB

128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147

QY

131 AGCATCTGCCAGCAGGAGACCTTCTGCTCTTTGCATTGGAAAAAATCTTCAGCAATTCC 190

DB

148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167

QY

191 CAGGAGCACCTGGATCTTCTCCAGCAGAGAATAAAACAGAGAGTTTCCCTCAGCAAAA 250

DB

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QY

251 GATGAATATCTGCAGACAGACATTTGGAGAGCTGTGTGAACCATTTGTATTCAACA 310

DB

188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207

QY

311 GATGTTGCCAAGCTCTCACTTTGGGCTTTCCCTCTCTCACTCTGATGACACCTCTCTCAAT 370

DB

208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227

QY

371 GAATTCCTCGAATATACACTCAACGACACCAAGATGCTTACACAGAAGAAGACAGAA 430

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QY

431 TTCGCTGTGTTGGAGGACAGAGGCTGAGCTCAGCGTCTCTCTGTTAAACAGAGATTC 490

DB

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QY

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QY

611 TTATAGACCAAGAAAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATC 670

DB

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QY

671 TTTAAGACACACAGTGCAGAGCAAAAAGCCCTCGAAGTGCACCTCTCTCTTTTATTTC 730

DB

328 AsnLysIleGluSerGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347

QY

731 AACAAAAATTGAAGTGAGGAAGTCTATCATGGAACCATGGAGGAGGACCAAGCAACAGAA 790

DB

348 IleTyrLeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGln 367

QY

791 ATCTATCTACAGCTACAGACTCAAAAGGCTGATCAGCAAGACNCTAGAGAGAGAACAA 850

DB

368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387

QY

851 TCTTTGGATGTGGGACAAATTCACTGATGAAATTTGCTGGATCACTGCCAGCCTTT 910

DB

388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407

QY

911 GGTCTCTGACCAATCACTGAGCTGCCCATCTTTTGTCTGTATTAACAGAGATGCTACT 970

DB

```
QY 408 LeuSerProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHis 427
DB 971 TTGAGTCCAGAACTTCCTCCTGTTGAACCCAGCTTGAGACAGTGGACGGAGACAGCAT 1030
QY 428 GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAla 447
DB 1031 GGTCTACCTGACACTTCCTGCTCCACCTGCTATGCGCTCTACCTCCCTGTCAGAACT 1090
QY 448 ProProPheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467
DB 1091 CCACCTTCCTTATGGCATCAAGCATCTCTCTGACTGATCAAGGCACACAGATACA 1150
QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSer 487
DB 1151 ATGGCCACTGACACAGCAATGCTAGTACAGGGCTCACCATCCACCATGATATTCT 1210
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArg 507
DB 1211 GCAATCAGCAACTGGCTCTGGGAATTCACATCCACCTGCATCTTCCAGATGACAGCGGA 1270
QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
DB 1271 TCAAGTGAGGTGGCGAGATATGCTCAGACACCTAGATGAATGGATCTCTCTGACACT 1330
QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
DB 1331 CTGTGCCCCATCTGAGGTACCGAGGCTCAGCGAATACGTTTCTGTCCAGATCAATTCCTTG 1390
QY 548 GluAspThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
DB 1391 GAGGATACCACTCCCTGCTCAGCTTTACAGTATATCACCACCTAGTCTTATGACCATGGCC 1450
QY 568 ProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
DB 1451 CCNAGGGCCGAGAGCTGTGTCTTCTCAGTCTGCGTGTGCTAACTAGCGCTTCTCC 1510
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGln 607
DB 1511 AACGACCTGTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAG 1570
QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
DB 1571 CTGCTGGTTCCATATCTACGATCCAACTTTACAGATTTAAGCAACTTGAATATCTTAAC 1630
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647
DB 1631 TTCAGAAACGGAGTGTGATTGTGAATACGAAATGAAGTTTGCTAAGTCTGTGCGGTAT 1690
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
DB 1691 AACCTCACCAGGCTGTGCACGGGGTCTTGGAGGATTTTCGTTCTGCTGCAGGCCCAAA 1750
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
DB 1751 CTCCATCTGGAATAGACAGCTACTCTCTCAACATTAACAGCTGATCAAGCAGATCCC 1810
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
DB 1811 TGCAAGTCTTCCTGCGCTCGCGCAATTTGCCAATGTGTGAAGAAGCAACGGACTGAGAA 1870
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
DB 1871 GCGAGTGTGCTGTGCAACACAGGATATGACCCAGGGAGGCTGAGCGGCTGGAAACA 1930
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
DB 1931 GGCCTCTGTGG - CTTGGCAAAAGGAATGCGAGGTCTCTCAGGAAAGGGAGCTCCATGCG 1989
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767
DB 1990 G--GTTCCAGATCACTCTGAAATCAAGCATACAAACCTAGTGTAA - AAGTTCAAAT 2046
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
```

```
DB 2047 CAACAAATACACAGTAAATCAGTAAAGAAATTCGTAATTACTACCGTAGAATGAA 2106
QY 788 GluPheAsnHisGlnAspTrpGluGlyAsn 797
DB 2107 GAATTTACCATCAAGATTGGGAGGAAT 2136

RESULT 9
AAA46329
ID AAA46329 standard; DNA; 2244 BP.
XX AAA46329;
AC
XX 04-SEP-2000 (first entry)
DT
XX
DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.
XX
XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
XX chromosome 6q13-q15; ocular disease; retinal detachment;
XX choriorretinal degeneration; retinal degeneration; cone degeneration;
XX age related macular degeneration; photoreceptor degeneration;
XX retinal pigment epithelium degeneration; mucopolysaccharidosis;
XX rod- cone dystrophy; cone-rod dystrophy; ss.
XX
OS Homo sapiens.
XX
XX WO2000026367-A2.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025440.
XX
XX 29-OCT-1998; 98US-00183972.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2000-365616/31.
XX
XX
XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
XX preventing, diagnosing and treating ocular disorders such as retinal
XX detachment and choriorretinal degeneration.
XX
XX Claim 3; Fig 19; 183pp; English.
XX
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an
XX additional intron after exon 5. The protein is an IPM component (IPMC).
XX Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX is located on chromosome 6q13-q15, between markers CHLC, GAT11F10 and
XX D6S284. The IPM proteins may be used to supplement a patient's own
XX production of the protein or to rectify alterations in their nucleic
XX acids that result in expression of an inactive protein. The IPM nucleic
XX acids may be used in this way to treat ocular diseases such as retinal
XX detachment, choriorretinal degeneration, retinal degeneration, age related
XX macular degeneration, photoreceptor degeneration, RPE (retinal pigment
XX epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
XX cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX also be used to assay for other modulators of IPM proteoglycan expression
XX and activity that may be used to treat ocular diseases. The nucleic acids
XX and proteins may also be used as diagnostic reagents to detect the
XX presence of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
XX
XX Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
```

```
Alignment Scores:
Pred. No.: 1,95e-259 Length: 2244
Score: 3323.00 Matches: 667
Percent Similarity: 95.56% Conservative: 0
Best Local Similarity: 95.56% Mismatches: 10
Query Match: 80.71% Indels: 23
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DB: 3 Gaps: 1  
US-10-007-270-2 (1-797) x AAA46329 (1-2244)  
QY 1 MetTyrLeuGluThrArgAlaAlaPheValPheThrIlePheLeuGlnValGlnGly 20  
DB 151 ATGATATTTGGAACTAGAGAGCTATTTTGGATTTTGGATTTTCCCAAGTTCAGGA 210  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
DB 211 ACCAAAGATATCTCCATTAACATATACCATCTGAACTAAGACATAGACAATNCCCA 270  
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
DB 271 AGAAATGAACAACTGAAGACTGAAATAATGACAAATGTCAACTATAGAGCAATA 330  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
DB 331 TTCGATTTGGCAAGNATCGAACAAGATCCGCAATTTTCCCAACGGGGTTAAAGTC 390  
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
DB 391 TGTCCACAGGAATCATGAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 450  
QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
DB 451 GTGTGTACAGGAAGCAGCATGGAGCATATCGATCTTCTGGATCGCATCCCTGACACA 510  
QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnThrPheCysLeuPheAspIle 140  
DB 511 GGGGAATATCAGGATCGGTGAGCATCTGCCAGCAGGAGACCTTCTGCCTCTTTGACATT 570  
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLysGln 160  
DB 571 GGAAAAAATCTTCAGCAATTCAGGAGCCTCGATCTTCTCCAGCAGAGAAATAAACAG 630  
QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
DB 631 AGAAGTTTCCCTGACAGAAAAAGATGAAATATCTGCAGAGAGACATTTGGGAGAGCTGGT 690  
QY 181 GluThrIleValIleSerThr----- 187  
DB 691 GAAACCATGTGCAATTTCAAC-AGCAATCTACATTTCAAGACTTGGGAGTATTTCTAAGA 749  
QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
DB 750 AAACCTTCAGAGAACCAATTCAGATGTTGCCAAGCTTCACTTGGGCTTTCCCTCTC 809  
QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
DB 810 ACTCCTGTATGACCCCTCCTCAATGGAATCTCGATATATACACTCAACGACACACAGATG 869  
QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
DB 870 CCTACAACAGAAAGAAACAGATTCCTGCTGTGTGGAGAGCAGAGGGTGGAGCTCAGC 929  
QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
DB 930 GTCTCTCTGTTAAACAGAGATTCAGGACAGAGTCTGCTGACTCCCACTCCCAATATTAC 989  
QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysValLeuProGly 279  
DB 990 CAGGAGCTAGCAGGAAGTCCCACTTCAGATGCAAAAGATATTATTAAGAACTTCCAGGA 1049  
QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
DB 1050 TTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAAAGATGGCTCAAGCTCC 1109  
QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
DB 1110 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGGCAAAAGCCCTGCA 1169  
QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339

RESULT 10  
ADA14844

DB 1170 AGTGACCTCTCTCTTTGATTCCCAACAAAATTTGAAGTGAAGAGTCTATCATGAAACC 1229  
QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
DB 1230 ATGGAGGAGACAAGCAACCAAGAAATCTATCTCACAGCTACAGACTCAAAAGGCTGATC 1289  
QY 360 SerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
DB 1290 AGCAAGCACTAGAGAAAGAACAAATCTTTGGATGTGGGACAATTCAGTCTCACTGATGA 1349  
QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
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QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
DB 1410 GCTGTTTATACAGAGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAACCCAGCTT 1469  
QY 420 GluThrValAspGlyValAlaGluHisGlyLeuProAspThrSerTyrSerProProAlaMet 439  
DB 1470 GAGACAGTGCAGAGAGAGAGATGCTTACCTGACACTTCTTGCTCTCCACTGCTATG 1529  
QY 440 AlaSerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeu 459  
DB 1530 GGCCT-ACCTCCCTGTGCAAGCTCCACCTTTCTTTATGGCATCAAGCATCTCTCTCTG 1588  
QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
DB 1589 ACTGATCAAGGACACACAGATCAATGGCCACTGACACAGCAATGCTAGTACAGGGCTC 1648  
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
DB 1649 ACCATCCCCACAGATGATTCTGCAATCAGCCAACTGGCTCTGGAAATTTCAATCCA 1708  
QY 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
DB 1709 CTTGCTCTTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGGATGGACAGACCTTA 1768  
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
DB 1769 GATGAATGGATCTGCTGACACTCTCTGCCCATCTGAGGTACAGAGCTCAGCGAATAT 1828  
QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
DB 1829 GTTTCCTGCCAGATCATTTCTTGGAGGATACCACTCTCTGTCTCAGCTTTACAGTATATC 1888  
QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeu 579  
DB 1889 ACCACTAGTTCTATGACCATTCGCCCAAGGGCCGAGAGCTGCTAGTGTCTTCTAGTCTG 1948  
QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
DB 1949 CGTGTGTCTTAACTGCTCTCCCAAGACCTGTTTCAACAGAGCTATTTGGAGTACCGA 2008  
QY 600 AlaLeuGluGlnGlnPheThrGlnLeuValProTyrLeuArgSerAsnLeuThrGly 619  
DB 2009 GCTCTGAGCAACAATTCACAGCTGTGTGTTCCATATCTACGATCCAATCTTACAGGA 2068  
QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
DB 2069 TTTAGCACTTGAATATCTTAACCTCAGAAACGGGAGTGTGATTTGTAATGACAAATG 2128  
QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659  
DB 2129 AAGTTTGTCAAGTCAAGTGCCTTAACCTCACCAAGGCTGTGCACGGGGTCTTTGAGGAT 2188  
QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677  
DB 2189 TTTCTGTTCTGTCAGCCCAACAATCCATCTGGAATAGACAGCTACTCTCTC 2242

ID ADAl4844 standard; cDNA; 2244 BP.  
 AC ADAl4844;  
 XX  
 XX  
 DT 06-NOV-2003 (first entry)  
 DE Human interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.  
 XX  
 XX ss; gene; human; IPMC 150 isoform C; gene therapy;  
 KW interphotoreceptor matrix component; IPMC; ocular disorder;  
 KW macular degeneration; photoreceptor death; retinal detachment.  
 XX  
 XX OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 151..747  
 FT FT /\*tag= b  
 FT FT /product= "IPMC 150 isoform C"  
 FT FT 151..200  
 FT FT sig\_peptide  
 FT FT /\*tag= a  
 FT FT /note= "Signal sequence"  
 FT FT 201..744  
 FT FT mat\_peptide  
 FT FT /\*tag= c  
 FT FT /note= "Mature IPMC 150 isoform C"  
 FT FT unsure 265..267  
 FT FT /\*tag= d  
 FT FT /note= "Encodes Pro"  
 FT FT unsure 346..348  
 FT FT /\*tag= e  
 FT FT /note= "Encodes His"  
 FT FT  
 XX US2002160954-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 XX 08-NOV-2001; 2001US-00007270.  
 PF  
 XX 29-OCT-1998; 98US-00183972.  
 PR  
 XX 29-OCT-1999; 99US-00430195.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX  
 XX Hageman GS, Kuehn MH;  
 PI  
 XX WPI; 2003-238235/23.  
 DR  
 XX P-PSDB; ADAl4845.  
 XX  
 XX New isolated or recombinant interphotoreceptor matrix component  
 FT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 FT treating or prognosticating ocular disorders, e.g. macular degeneration  
 FT or retinal detachment.  
 PT  
 XX  
 XX Claim 3; Page 36-37; 76pp; English.  
 PS  
 XX  
 XX The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform C.  
 XX  
 XX Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 1,95e-259 Length: 2244  
 Score: 3323.00 Matches: 667  
 Percent Similarity: 95.56% Conservative: 0  
 Best Local Similarity: 95.56% Mismatches: 10  
 Query Match: 80.71% Indels: 23

DB: 7 Gaps: 1  
 US-10-007-270-2 (1-797) x ADAl4844 (1-2244)  
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 Db 151 ATGTAATTGGAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGGA 210  
 Qy 21 ThrLysAspIleSerIleLeuThrHisSerGluThrLysAspIleAspIleAspIleAspIle 40  
 Db 211 ACCAAAGATATCTCCATTACCATATACCATCTCGAACTAAAGACATACCAATNCCCAC 270  
 Qy 41 ArcAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 Db 271 AGAANTGAACAACCTGAAAGTACTGAAAAAATGTCAAAATGTCAACTATGAGAGCAATA 330  
 Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValValVal 80  
 Db 331 TTCGATTTCGCAAGNATCGAACAAAAAGATCCGATTTTCCCAACGGGGTTAAAGTC 390  
 Qy 81 CysProGlnLysSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 391 TGTCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 450  
 Qy 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 451 GTGTGTCCAGGAACGACGATGGGAAGCATATCGATCTTCTCGATCGCATCCCTGACACA 510  
 Qy 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 511 GGGGAATATCAGGACTGGGTGACATCTCCAGCAGGAGACCTTCTGCCTCTTTTGACATT 570  
 Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160  
 Db 571 GGAATAAACTTCAGCAATTCACAGGAGACCTGGATCTTCTCCAGCAGAGATAAAACAG 630  
 Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluProGly 180  
 Db 631 AGAAGTTTCCTGCACAGAAAAGATGAATATCTGCAGAGAAGACATTGGGAGAGCCTGT 690  
 Qy 181 GluThrIleValIleSerThr----- 187  
 Db 691 GAAACCATTTGTCTATTTCAC -AGCAATCTACATTTCAAAGACTTGGGCAGTATTCTAAGA 749  
 Qy 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 Db 750 AAACCCCTCAGACAGACAAATTCAGATGTTCACAGTCTCACTTGGGCTTTCCCTCTC 809  
 Qy 200 ThrProAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 Db 810 ACTCCTGATGACACCTCCTCAATGGAAATCTCGATAATACACTCAACGACCAAGATG 869  
 Qy 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSer 239  
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 Db 930 GTCTCTCTGTGTAACCAAGATTCAAGGAGAGCTCGCTGACTCCAGTCCCATATTAC 989  
 Qy 260 GlnGluLeuAlaGlyLysSerGlnLeuMetGlnLysIlePheLysLysLeuProGly 279  
 Db 990 CAGAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAACTTCACAGA 1049  
 Qy 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
 Db 1050 TTCAAAAAATCCATGTGTAGGATTAGACCAAAAGAAAAAGATGGCTCAAGCTCC 1109  
 Qy 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 Db 1110 ACAGAGATGCACTTACGGCCATCTTTAAGAGACACAGTGCAGACCAAAAGCCCTGCA 1169  
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Qy 360 SerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379
Db 1290 AGCAAGCACTAGAGGAGGAGCAATCTTTGGATGTGGGCAATTCAGTTCACCTGATGAA 1349
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Db 1350 ATTGCTGATCACTGCCAGCTTTGGTCTTGACACCAATCAGAGCTGCCACATCTTTT 1409
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Qy 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMet 439
Db 1470 GAGACAGTGGACGAGGAGAGCATGTTCTACCTGACACTTCTTGCTCTCCACTGCTATG 1529
Qy 440 AlaSerThrSerLeuSerGluAlaProPhePheMetAlaSerIlePheSerLeu 459
Db 1530 GCCCT-ACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAGACATCTTCTCTCTG 1588
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Db 1589 ACTGATCAAGGCACACAGATACAAATGCCACTGACCAATGCTAGTACAGGGCTC 1648
Qy 480 ThrIleProThrSerAspTyrluSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499
Db 1649 ACCATCCCAACAGTGATTTATCTGCAATCAGCCAACTGGCTCTGGGAATTCACATCCA 1708
Qy 500 ProIaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519
Db 1709 CCTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGTATGGACAGACCTA 1768
Qy 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrl 539
Db 1769 GATGAAATGGATCTGTCTGACACTCTGCCCCATCTGAGGTACAGAGCTCAGCGATAT 1828
Qy 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrlle 559
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Qy 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPheSerLeu 579
Db 1889 ACCACTAGTCTATGACCAITGGCCCCCAAGGGCCGAGAGCTGGTGTGTTCTTCAGTCTG 1948
Qy 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrlArg 599
Db 1949 CGTGTGTCTAATGCGCTCTTCCACAGACCTGTTTCAACAGAGCTATTTGGAGTACCGA 2008
Qy 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrluArgSerAsnLeuThrGly 619
Db 2009 GCTCTGGAGCAACAATTCACACAGCTGCTGTGTTCCATATCTACGATCCAACTCTACAGGA 2068
Qy 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639
Db 2069 TTTAAGCAACTTGAATACTTAATCTTCAAAACGGGAGTGATGTGATGAAATGCAAAATG 2128
Qy 640 LysPheAlaLysSerValProTyrluAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659
Db 2129 AAGTTTGTAAGTCAGTCCGCTATAAACCCTCAACAGGCTGTGACCGGGTCTTTGGAGAT 2188
Qy 660 PheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrlSerLeu 677
Db 2189 TTTGCTTCTGTGAGCCCAACAACTCCATCTCGAAATAGACACTACTCTCTC 2242
RESULT 11
ACC57948
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ACC57948 standard; cDNA; 2244 BP.
ACCS7948;
11-AUG-2003 (first entry)
Human interphotoreceptor matrix IPM 150, isoform C, cDNA.
Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
receptor; ophthalmological; gene therapy; gene; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 151..747
FT /*tag= a
FT /product= "IPM 150"
FT sig_peptide 151..210
FT /*tag= b
FT FT 265..267
FT /*tag= c
FT /note= "encodes Pro"
FT FT 346..348
FT /*tag= d
FT /note= "encodes His"
PN WO2003039346-A2.
PD 15-MAY-2003.
PF 08-NOV-2002; 2002WO-US036090.
PR 08-NOV-2001; 2001US-00077270.
XX (IOWA ) UNIV IOWA RES FOUND.
XX Hageman GS, Kuehn MH;
PI WPI; 2003-441440/41.
DR P-PSDB; ABR42344.
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
treating or preventing photoreceptor death or retinal detachment, or for
treating ocular disorders.
Claim 1; Page 79-80; 105pp; English.
XX The present sequence is that of cDNA encoding isoform C of novel human
interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
is located on chromosome 6q13-q15, a region that also contains loci for
progressive bifocal choriorretinal atrophy, autosomal dominant Stargardt's
-like macular dystrophy, North Carolina macular dystrophy and Salla
disease. Members of the IPMC gene family have been identified in humans,
monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
antibodies that specifically bind the polypeptides, and vectors
comprising the polynucleotides. A claimed method of treating or
preventing photoreceptor death or retinal detachment involves
administering an IPMC polynucleotide, polypeptide or antibody. Also
claimed is a method for identifying a compound capable of modulating IPMC
gene expression
XX
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
Alignment Scores:
Pred. No.: 1,958-259 Length: 2244
Score: 3323.00 Matches: 667
Percent Similarity: 95.56% Conservative: 0
Best Local Similarity: 95.56% Mismatches: 10
Query Match: 80.71% Indels: 23
DB: Gaps: 1
```



US-10-007-270-2 (1-797) x ACC57948 (1-2244)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly 20  
Db 151 ATGTATTTGGAAATCAGAGAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGGA 210  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
Db 211 ACCAAAGATATCTCCATTAAACATATACCATTTCTGAACATAAGACATAGACAATNCCCA 270  
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
Db 271 AGAATGAACAACTGAAGTACTGAAAAATGTACAAAATGTCAACTATGAGACGATA 330  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
Db 331 TTCGATTTGGCAAGNATCGAACAACAAAGATCCGCAATTTTCCCAACGGGGTTTAAAGTC 390  
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
Db 391 TGTCACACAGGAATCCATGAAACAGATTTTACACAGTCTTCCAGCTTATTATAGATTGAGA 450  
QY 101 ValCysGlnGluAlaValIleGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
Db 451 GTGTCTCAGGAAGCAGCATGGAGCATATCGGATCTTTCTGGATCGCATCCCTGACACA 510  
QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
Db 511 GGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTTGACATT 570  
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
Db 571 GGAATAAACTTCAGCAATTTCCAGGAGCACCTGGATCTTCTCCAGCAGAGATAAACAAG 630  
QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
Db 631 AGAAGTTTCCCTGCAGAGAAAAGATGAATATCTGCAGAGAGACATTTGGGAGCCCTGGT 690  
QY 181 GluThrIleValIleSerThr----- 187  
Db 691 GAAACCAATGTCTTCAAC-AGCAATCTACATTTCAAGACTTGGGCAGTATTCTAAGA 749  
QY 188 -----AspValAlaIleValSerLeuGlyProPheProLeu 199  
Db 750 AAACCCCTCAGAGAGCAAAATTCAGATGTTGCCACGTCTCACTTGGGCTTTTCCCTCTC 809  
QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
Db 810 ACTCTGATGACACCTCTCTCAATGGAATTTCTCGATAATACACTCAACGACACCAAGATG 869  
QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
Db 870 CCTACAACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGAGCAGAGGGTGGAGTCAAGC 929  
QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
Db 930 GTCTCTCTGGTAAACAGAAAGTTCAAGGACAGCTCGCTGACTCCAGTCCCAATATTAC 989  
QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
Db 990 CAGGAGCTAGCAGGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGA 1049  
QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
Db 1050 TTCAAAAAATCCATGTGTGTAGATTTTAGACCAAAAGAAAGAAAGATGGGTCAAGCTCC 1109  
QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
Db 1110 ACAGAGATCCAACTTACGGCCATCTTTTAGACACACAGTCAGAGAGCAAAAAGCCCTGCA 1169  
QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339

RESULT 12  
ADA14847  
ID ADA14847 standard; cDNA; 3668 BP.

Db 1170 AGTGACCTCTCTCTTTGATTCCAAACAAATTGAAAGTGAGGAAGTCTATCATCGAACC 1229  
QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
Db 1230 ATGGAGGAGACAAAGCAACCAAAATCTATCTCACAGCTACAGACCTCAAAAGGCTGATC 1289  
QY 360 SerLysAlaLeuGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
Db 1290 AGCAAGACACTAGAGAGACAACTTTGGATGTGGGACAAATTCAGTTCACATGATGA 1349  
QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
Db 1350 ATTGCTGGATCATCTCGACGCTTTGGTCTCTGACACCAATCAGAGCTGCCACATCTTT 1409  
QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
Db 1410 GCTGTTATACAGAGATGCTACTTTGAGTCCAGAACTTCTCTCTGTGAACCCAGCTT 1469  
QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrSerProProAlaMet 439  
Db 1470 GAGACAGTGGACGGAGCAGAGCATGGTCTACCTGACACTTCTTGTCTCCACCTGCTATG 1529  
QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
Db 1530 GGCCT-ACCTCCCTGTGAGAGCTCCACCTTTCTTATGGCATCAGCATCTTCTCTCTG 1588  
QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
Db 1589 ACTGATCAGGACACACAGATACATGGCCACTGACACGACAAATGCTAGTACAGGCTC 1648  
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyLysSerHisPro 499  
Db 1649 ACCATCCCAACAGTGAATTTATCTGCAATCAGCCAACCTGGCTCTGGGAATTTCAATCCA 1708  
QY 500 ProAlaSerSerAspAspSerArgSerAlaGlyGlyGluAspMetValArgHisLeu 519  
Db 1709 CTTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGTATGGACAGACCTA 1768  
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
Db 1769 GATGAATGGATCTGTCTGACACTCTGCCCCATCTGAGGTACCGAGAGCTGCTAGTGTCTT 1828  
QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
Db 1829 GTTCTGTCCCAGATCATTTCTTGAGGATACCATCTCTGCTCAGCTTACAGTATATC 1888  
QY 560 ThrThrSerSerMetThrIleAlaProLysGlyA-gGluLeuValValPhePheSerLeu 579  
Db 1889 ACCACTAGTCTTATGACCATTTGCCCCCAAGGCGGAGAGCTGGTAGTGTCTTCACTCTG 1948  
QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
Db 1949 CGTGTGTAAACATGGCCTTCTCCAAACGACCTGTTCACCAAGAGCTATTGGAGTACCGA 2008  
QY 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619  
Db 2009 GCTCTGGACCAACATTCACACAGCTGCTGGTTCCTATATCTACGATCCCAATCTTACAG 2068  
QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
Db 2069 TTTAAGCAACTTGAATACTTAACCTTCAAGAAACGGAGTGTGATTGTGAATAGCAAAATG 2128  
QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659  
Db 2129 AGTTTGTAAAGTCAGTCCGCTATTAACCTCACCAAGGCTGTGCACGGGTCTTGGAGGAT 2188  
QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677  
Db 2189 TTTCTGTCTGTGACGCCCAACCAACTCCATCTGGAATAGACAGACTACTCTCTCTC 2242

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XX AC ADA14847;
XX DT 06-NOV-2003 (first entry)
XX DE Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX KW ss; gene; mouse; IPMC 150 isoform A; gene therapy;
XX KW interphotoreceptor matrix component; IPMC; ocular disorder;
XX KW macular degeneration; photoreceptor death; retinal detachment.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT 196..2592
XX FT /*tag= a
XX FT /product= "IPMC 150 isoform A"
XX PN US2002160954-A1.
XX XX
XX PD 31-OCT-2002.
XX XX
XX PF 08-NOV-2001; 2001US-00007270.
XX XX
XX PR 29-OCT-1999; 98US-00193972.
XX PR 29-OCT-1999; 98US-00430195.
XX XX
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX XX
XX PI Hageman GS, Kuehn MH;
XX DR WPI; 2003-238235/23.
XX DR P-PSDB; ADA14848.
XX PT New isolated or recombinant interphotoreceptor matrix component
XX PT polynucleotide and polypeptide, useful for diagnosing, preventing,
XX PT treating or prognosticating ocular disorders, e.g. macular degeneration
XX PT or retinal detachment.
XX PS Claim 3; Page 39-41; 76pp; English.
XX CC The invention relates to an isolated or recombinant interphotoreceptor
XX CC matrix component (IPMC) polynucleotide. Also disclosed is a vector
XX CC comprising a promoter of an interphotoreceptor matrix component (IPMC)
XX CC gene operatively linked to the IPMC polynucleotide. The IPMC
XX CC polynucleotides, polypeptides and antibodies are useful for diagnosing,
XX CC preventing, treating or prognosticating ocular disorders, e.g. macular
XX CC degeneration, photoreceptor death or retinal detachment. They are also
XX CC useful for identifying a compound capable of modulating IPMC gene
XX CC expression in a cell. The present sequence represents cDNA encoding mouse
XX CC interphotoreceptor matrix component, IPMC, 150 isoform A.
XX SQ Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 2,37e-196 Length: 3668
Score: 2548.50 Matches: 528
Percent Similarity: 75.12% Conservative: 79
Best Local Similarity: 65.35% Mismatches: 180
Query Match: 61.90% Indels: 21
DB: 7 Gaps: 9

US-10-007-270-2 (1-797) x ADA14847 (1-3668)
QY 1 MetTyrLeuGluThrArgAlaGlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
Df : : : : :
Db 196 ATGAATTTTCAATTAACATGCTATCTTTTGGGATTTTCTCCAGATTCAAGGA 255
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Df : : : : :
Db 256 ATCAAGATACCTCTATTAAATATTCAGTCTGAATTAATAAATAGACAAACCCCA 315
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60

316 AGAATCGAAACAACTTGAAGTACTTCAACAGTGCACAAAGTGTCAACCATGAACGAATA 375
61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
376 TTTCGATTTCGAAAGCTTCGAAACCAAGATCAGCAGCTTTTCCCA---GCTGCTAACATC 432
81 CysProGlnGlnSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
433 TGCCACAGGAATCTCTTGAGACAGATTTTGAAGTCTTCAAGATATTATATGACTGAGA 492
101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
493 GTATGTCAAGAAAGTCTGTGGGAAGCATATCTATCTTTCTGCAGCGAATTCCTGACACA 552
121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140
553 GAGGAATATCAAGACTGGGTCTGCGCAAGAAACCTTCTGCTCTTTGACATT 612
141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160
613 GGGAAAAAATTTCAGCAACTCCCGAGGACCTAGATCTTCTTCAGCAGAGATAAAGACAG 672
161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
673 AGAAGCTTCCCTGGGAGGAAAGATGAGACAGCGCTCCATGGAGACACTTGAAGCACCTACT 732
181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
733 GAAGCCCTGTGTACCCACAGATGTTTCCAGGATGTCTCTGGGGCCCTTCCACATTCTCT 792
201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
793 TCTGATGACACAGACCTCAAGGAGATTCTCAGTGTCCACCTCAAGCAGACATTCAAAAGCC 852
221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGlnGln 234
853 ACAACAGAAAGTAAACACAGAACCTATTACGTTGTCTGAATTTCTCA-----TCAGAGGAG 906
235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254
907 AGGTGGAATTCAGCATCTCTCTGCCAACACAGGTTCAAGGCAGAGCTCAACCACTCT 966
255 GlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274
967 GGGTCACCATATACAGGAACTGGTGGACAGTCCCACTGTCAGTTGCAAAAGATATT 1026
275 LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGlyLys 294
1027 AGAAACTTCCAGGATTCGAGAAATCCGTGATTAGGATTTAGACCAAGAAAGAAAGAA 1085
295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314
1087 GATGGTTCAGGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGAGACCATCAGAA 1146
315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334
1147 GCAAAAAGCCCTGATGATCATCTCTCTTGTATTCACACAAATTTGAAAGTGAAGA 1206
335 ValTyrHisGlyThrMetGluLysGlnProGluIleTyrLeuThrAlaThrAsp 354
1207 ATCCATCATGGAGTCATA--GAAGACAAACCAACAGAAACCTACCTCACAGCTACAGAC 1263
355 LeuLysArgLeuIleSerLysAlaLeuGluGlnGlnSerLeuAspValGlyThrIle 374
1264 CTCAAAAAATCATCATCACTACTAGATGGAGCCTGTCTCTGTGTAGAGGGGAAATTT 1323
375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394
1324 CCATTCGGTGTAGAGTTACTGGACACTC-----TTCAGACCTGTCTCACTGACACAGAT 1377
395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414

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Db 1378 CTGCCCAAGCCCTTCTGATGTCACAGAGGATGCCACTTGTGAGTCCAGAACTTCCTTC 1437  
Qy 415 ValGluProGluLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430  
Db 1438 GTTAGCCTAGGCTTGAGGAGTGGACAGAGAAGAGATCTGAGCTGCTGGAATGCTCCTC 1497  
Qy 431 ---AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
Db 1498 AAGACAGTCTTGCTGCTCCTGATGATGCTCAATTTCCGATCAGAAATCTACT 1557  
Qy 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
Db 1558 TCGTTT---ACACCTAGCATCTCTCTAGATGCTCAAAGCCCTCCCTTGATGACC 1614  
Qy 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspThrSerAlaIle 489  
Db 1615 ACTGGCCCAACAGCATCTATCCCAAGCCCATCTCTCCCACTATGATTTCTACCATC 1674  
Qy 490 SerGlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerArgSerSer 509  
Db 1675 CGCCAATTGCTCTGGAATCGTCACATTTGCTGATGCTCAAGCCCTCCCTTGATGACC 1734  
Qy 510 AlaGlyGlyLeuAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
Db 1735 ACAAGCAGGCATGACACAAATCCGAGACCTAGATGGCATGCTGTCTGACACGCCGCC 1794  
Qy 530 ProSerGluValProGluLeuSerGluTyValSerValProAspHisPheLeuGluAsp 549  
Db 1795 TTCTCAGAATATCAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1854  
Qy 550 ThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAlaProIlys 569  
Db 1855 ACCACACCCATCCCAACAGTTCATGATGATGATGATGATGATGATGATGATGATGAT 1914  
Qy 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589  
Db 1915 GGCAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1974  
Qy 590 LeuPheAsnIlySerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
Db 1975 CTGTTCAACAAGATGCTCTGAGATATCAAGCCCTGGAACACGATTCACAGACCTGCT 2034  
Qy 610 ValProTyLeuArgSerAsnLeuThrGlyPheLeuGlnLeuGluLeuLeuAsnPheArg 629  
Db 2035 GTTCCCTATCTACGATCGAATCTTCGGGATTTAGCAATCGAAATCTCAGTTCAGA 2094  
Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyAsnLeu 649  
Db 2095 AACGGAAGTGTGATGTCGACACCAAGTCCGCTTTCGAAGCGGTACCTTACACCTC 2154  
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
Db 2155 ACCGAGCCCTGCGCGGGTCTTGGAGGATCTTCGGTCCACCGCATCTCAAGGGCTCAAT 2214  
Qy 670 LeuGluIleAspSerTySerLeuAsnIleGluProAlaAspGlnAlaAspProCysIlys 689  
Db 2215 CTGGAATCGAAGACTACTCTCCGATGATGATGATGATGATGATGATGATGATGATGAT 2274  
Qy 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
Db 2275 CTCCTAGCTGTGGCAATTTGCCAGTGTGTAAGAATGATGTCGACAGAGGAAGCAGAG 2334  
Qy 710 CysArgCysLysProGlyTyArgSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729  
Db 2335 TGTGCTGTCAGACAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2394  
Qy 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
Db 2395 TGTCCCTCTGGA---AAGACTTGTGGCGCGCGGAGAACACCACTCCATGACGCCA 2451  
Qy 750 ProAspHisSerGluAsnGlnAlaTyLysThrSerValLysLysPheGlnAsnGlnGln 769  
Db 2452 CCAGATCACTCTAAACCAAGCTCAGGAACCTGGTGTAAAAAGCTA-----CGTCAG 2505

Qy 770 AsnAsnIysValIleSerLysArgAsnSerGluLeuThrValGluTyArgGluPhe 789  
Db 2506 CAAATATAGTAGTCAAGAAAGAAATTTCAAACATATAGTATAGTATTTGAAGAATTT 2565  
Qy 790 AsnHisGlnAspTrpGluGlyAsn 797  
Db 2566 GAAGACAGGACTGGGAGGAAT 2589  
RESULT 13  
ACC57950  
ID ACC57950 standard; cDNA; 3668 BP.  
XX ACC57950;  
AC ACC57950;  
DT 11-AUG-2003 (first entry)  
XX Mouse interphotoreceptor matrix IPM 150, isoform A, cDNA.  
DE Mouse; interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;  
XX ophthalmological; gene therapy; gene; ss.  
KW Mus sp.  
OS  
FH Key Location/Qualifiers  
CDS 196..2592  
FT /\*tag= a  
FT /product= "IPM 150"  
XX  
XX WO2003039346-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 08-NOV-2002; 2002WC-US036090.  
XX  
XX 08-NOV-2001; 2001US-00077270.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX WPI; 2003-441440/41.  
XX P-PSDB; ABR42345.  
XX  
XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
XX treating or preventing photoreceptor death or retinal detachment, or for  
XX treating ocular disorders.  
XX  
XX Claim 1; Page 81-82; 105pp; English.  
XX  
XX The present sequence is that of cDNA encoding isoform A of novel mouse  
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
XX is located on chromosome 9. Members of the IPMC gene family have been  
XX identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and  
XX rat. 2 Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or  
XX IPM2). The invention provides IPM 150 and IPM 200 polynucleotides and  
XX polypeptides, antibodies that specifically bind the polypeptides, and  
XX vectors comprising the polynucleotides. A claimed method of treating or  
XX preventing photoreceptor death or retinal detachment involves  
XX administering an IPMC polynucleotide, polypeptide or antibody. Also  
XX claimed is a method for identifying a compound capable of modulating IPMC  
XX gene expression  
XX  
XX Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;  
SQ  
Alignment Scores:  
Pred. No.: 2,37e-196 Length: 3668  
Score: 2548.50 Matches: 528  
Percent Similarity: 75.12% Conservative: 79  
Best Local Similarity: 65.35% Mismatches: 180  
Query Match: 61.90% Indels: 21  
Gaps: 9  
DB:

Db	1207	ATCATCATGGAGTCATA---GAAGACAAACACACGAAACCTTACCTCAGCTCAGCTACAGAC	1267
Qy	355	LeuLyArgLeuIleSerLySAlaLeuGluGluGluGlnSerLeuAspValGlyThrile	374
Db	1264	CTCAAAAACTCATCATCAACTACTAGATGGAGACAGCTGCTCTGGTAGAAGGGAATAAT	1323
Qy	375	GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu	394
Db	1324	CCATTCGGTGATGAAGTTACTGGGCACTC-----TTCAGACCTGTCACTGACACGAGT	1377
Qy	395	LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro	414
Db	1378	CTGCCAAGCCCTTGCTGTATGTCACAGAGATGCCACTTTGAGTCAGAACTTCCTTC	1437
Qy	415	ValGluProGlnLeuGlnThrValAspGlyAlaGluHisGlyLeuPro-----	430
Db	1438	GTTGAGCCTAGGCTGAGGCAGTGGACAGAGAAGGATCTGAGCTGGATGTGGAATGTCTCTCC	1497
Qy	431	---AspThrSerTyrProProAlaMetAlaSerThrSerLeuSerGluAlaProPro	449
Db	1498	AAAGACAGTTCTTGGTCTCCACCTGTATCAGCCCTCAATTCCCGATCAGAAAAATCTACCT	1557
Qy	450	PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla	469
Db	1558	TCGTTT---ACACCTAGCATCTTCTCTAGATGCTCAAAGCCGCCCTCCTCTGATGACC	1614
Qy	470	ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle	489
Db	1615	ACTGGGCCAACAGCATCTATCCCCAAGCCCACTCTCCCACTATCATGATATTCTACCATC	1674
Qy	490	SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSerSer	509
Db	1675	CGCAATTGCTCTGGAATCGTCACATGGCTTGCATCTCTCCAGTCACAGAGAGCTGATC	1734
Qy	510	AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla	529
Db	1735	ACAAGCAGCCATGACACAAATCCGAGACCTAGATGGCATGGATGTGCTGACAGCCAGCC	1794
Qy	530	ProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAsp	549
Db	1795	TTGTCAGAAATATCAGAACTGAGTGGATACGATTCGCTCGGTCAGTTCTTTGGAGATG	1854
Qy	550	ThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLys	569
Db	1855	ACCACACCCATCCCAACAGTACGTTGGTTCATCACACAGCTCCGAGACCAATGGCCACCAAG	1914
Qy	570	GlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp	589
Db	1915	GGCCAGAGTAGTGGTATTCTTCAGCCTGGGTGTGCTTAACATGCGTTCCTCTATGAC	1974
Qy	590	LeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu	609
Db	1975	CTGTTCAACAAGAGTTCTCTGGAGTATCAAGCCCTGGAAACAAGANTTCAAGACCTGCTG	2034
Qy	610	ValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg	629
Db	2035	GTTCCCTATCTAGATCGAATCTTACGGATTTAAGCACTGGAAATATCTCAGCTTCAGA	2094
Qy	630	AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu	649
Db	2095	AACGGAAGTGTGATCGTGAACAGCAAAGTCGGTGTTCGAAAGCGGTACCTTCAACCTC	2154
Qy	650	ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis	669
Db	2155	ACCAGGCCCTGCGCGGGTCTTGGAGGATCTTTCGGTCCACCGAGCTCAAGGGCTCAAT	2214
Qy	670	LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys	689
Db	2215	CTGGAATCGAAGCTACTCCTCTCGACATTGAACCAAGCTGATCAGCGGATCCTCTGCAA	2274
Qy	690	PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu	709
Db	2275	CTCTACAGCTGTGGCAAAATTTGCCAGTGTGTAAAGAATGAGTGGACAGAGGACGAGAG	2334

QY 710 CysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729  
 DB 2335 TGTGCGTGCAGACAGGACATGAGCCACGAGACCGCTGACCTACAGACCCCTGAACCTC 2394  
 QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
 DB 2395 TGTCCCCCTGGA---AAGACTTGTGTGGCGCGCGGAAACAGCACTCATGCGAGGCCA 2451  
 QY 750 ProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsnGlnGln 769  
 DB 2452 CCAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTAAAGGCTA-----CGTCAG 2505  
 QY 770 AsnAsnLysValLysSerLysArgAsnSerGluLeuLeuThrValGluTyrGluGluPhe 789  
 DB 2506 CAAATTAAGGTAGTCAAGAAAGAAATCTTAACCTATGCTATAGGATTGAAGAATT 2565  
 QY 790 AsnHisGlnAspTyrGluGlyAsn 797  
 DB 2566 GAAGACAGGACCTGGGAGGGAAT 2589

## RESULT 14

AAA46309  
 ID AAA46309 standard; cDNA; 3206 BP.

AC AAA46309;

DT 04-SEP-2000 (first entry)

XX cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).

XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KW chromosome 6q13-q15; ocular disease; retinal detachment;  
 KW chorioretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod- cone dystrophy; cone-rod dystrophy; ss.

XX Mus sp.

PH Key Location/Qualifiers

FT 1. .2130  
 FT /\*tag= a  
 FT /transl\_except= (pos: 16. .18, aa: Val)  
 FT /transl\_except= (pos: 55. .57, aa: Ala)  
 FT /transl\_except= (pos: 58. .60, aa: Tyr)  
 FT /transl\_except= (pos: 73. aa: Asp)  
 FT /transl\_except= (pos: 234. .236, aa: Xaa)  
 FT /transl\_except= (pos: 271. .273, aa: Xaa)  
 FT /transl\_except= (pos: 403. .405, aa: Xaa)  
 FT /transl\_except= (pos: 2107. .2109, aa: Xaa)  
 FT /product= "interphotoreceptor matrix proteoglycan IPM150"  
 FT /note= "Xaa is an unspecified amino acid"

XX WO200026367-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025440.

XX 29-OCT-1998; 98US-00183972.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2000-365616/31.

XX P-PSDB; AAY93338.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 preventing, diagnosing and treating ocular disorders such as retinal  
 detachment and chorioretinal degeneration.

XX

PS Claim 2; Fig 6A; 183pp; English.

XX The present sequence encodes an interphotoreceptor matrix (IPM)  
 CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).  
 CC Two subfamilies of IPMs, IPM150 and IPM200, exist. The human IPM150 gene  
 CC is located on chromosome 6q13-q15, between markers CHLC.GA11P10 and  
 CC D6S284. The IPM proteins may be used to supplement a patient's own  
 CC production of the protein or to rectify alterations in their nucleic  
 CC acids that result in expression of an inactive protein. The IPM nucleic  
 CC acids may be used in this way to treat ocular diseases such as retinal  
 CC detachment, chorioretinal degeneration, retinal degeneration, age related  
 CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
 CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
 CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
 CC also be used to assay for other modulators of IPM proteoglycan expression  
 CC and activity that may be used to treat ocular diseases. The nucleic acids  
 CC and proteins may also be used as diagnostic reagents to detect the  
 CC presence of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies

SQ Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;

## Alignment Scores:

Pred. No.: 1.57e-167 Length: 3206  
 Score: 2192.00 Matches: 457  
 Percent Similarity: 74.08% Conservative: 69  
 Best Local Similarity: 64.37% Mismatches: 164  
 Query Match: 53.24% Indels: 20  
 DB: 3 Gaps: 8

US-10-007-270-2 (1-797) x AAA46309 (1-3206)

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 QY 119 AspThrGlyGluTyrGlnAspTyrPheValSerIleCysGlnGlnGluThrPheCysLeuPhe 138  
 DB 85 GACACAGAGGAATATCAAGGCTGGTCTGAGCTCTGCCAGAGAAACCTCTTGCCTCTTT 144  
 QY 139 AspIleGlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgile 158  
 DB 145 GACATTGGGAAAAAATCTGAGCACTCCAGAGACCTAGATCTTCTTCAGCAGAGATA 204  
 QY 159 LysGlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGlu 178  
 DB 205 AAACAGAGAGCTTCCCTCGGAGGAAAGATGWGACAGCCTCCATGGAGACACTGGAAGCA 264  
 QY 179 ProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPhePro 198  
 DB 265 CCTACTGRAGCCCTGTGGTACCCACAGATGTTTCCAGGATGTCCTGGGGCCMTCCCA 324  
 QY 199 LeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLys 218  
 DB 325 CTTCCTTCTGATGACACAGACCTCAAGAGATCTTCAGTGTCCACCTCAAGGACATTCAA 384  
 QY 219 MetProThrThrGluArgGluThr-----GlupheAlaValLeuGlu 232  
 DB 385 AAGCCCAACACAGAAAGTAAACACCACTTTCATCAVGTGTCTGAATTTCTCA-----TCA 438  
 QY 233 GluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAla 252  
 DB 439 GAGGAGAGGTGGATTTCAGCATCTCTCTGCCAAACACACAGGTTCAAGGCAGAGCTCACC 498  
 QY 253 AspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLys 272  
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 QY 273 IlePheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLys 292  
 DB 559 ATATTTAAGAAACTTCCAGGATTCGGAGAAATCCGTGTATTAGATTATAGCCAAAGAAA 618  
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Qy 333 GluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAla 352
Db 739 GAAAGAAATCCATCATGGAGTCATA--GAAGACAAACCAACCAAGAACCTTACCTCACAGCT 795
Qy 353 ThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGly 372
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Qy 373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392
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Qy 393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412
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Qy 413 ProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430
Db 970 CTTTCGTTGAGCTAGCTAGCTTGGAGCAGTGGACAGAGAGGATCTGAGCTGCTGGAATG 1029
Qy 431 -----AspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAla 447
Db 1030 TCTCTCAAGACAGATGTTCTGGTCTCCACCTGTATCAGCCTCAATTTCCCGCATCAGAAAT 1089
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Qy 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487
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Qy 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
Db 1267 CTGATCACAAGCAGCCATGACAACTCCGAGACCTAGATGGCATGGATGTGTCTGACAGC 1326
Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
Db 1327 CCAGCCTTGTCAAGAAATATCAGAACTGAGTGGATACGATTCTGCTCGGGTCAGTCTCTG 1386
Qy 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
Db 1387 GAGATGACCACACCCATCCCAACAGTACGGTTTCATCACCACCGCTCCGAGACCATTC 1446
Qy 568 ProLysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db 1447 ACCAAGCGCCAGAGAGTAGTGTATCTTCAGCCTGCTGCTGCTAAACATGCGCTCTCC 1506
Qy 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607
Db 1507 TATGACCTGTTCAACAGAGTCTCTGGAGTATCAAGCCCTGGACACGATTCACAGAC 1566
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Qy 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647
Db 1627 TTCAGAAACGGAAGTGTGATCGTGAACAGCAAGTCCGGTTTGCAAGCGGTACCTTAC 1686
Qy 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
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Db 1747 CTCAATCTGGAATCGAAAGACTACTCCTCGACATTGAACCGACTGATCAGCGGATCCC 1806
Qy 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
Db 1807 TGCAAACTCTTAGACTGTGGCAAAATTTGCCAGTGTGTAAAGAATGATGTGACAGAGAA 1866
Qy 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db 1867 GCAGAGTGTCTCGACAGACAGGACATGAGAGCCACCGGACCTGGACTACCAGACCTG 1926
Qy 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db 1927 AACCTCTGTCCCTCGGA--AAGACTTGTGTGGCGCGGAGAACCAAGCAACTCCATGC 1983
Qy 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767
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Qy 768 GlnGlnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
Db 2038 CGTCAGCAAAATAAGGTAGTCAGAAAGAAATTTCTAACTATCAGCTATAGGATTTGAA 2097
Qy 788 GluPheAsnHisGlnAspTyrGluGlyAsn 797
Db 2098 GAATTTGAARACCAGGAGCTGGGAGGAAAT 2127

RESULT 15
ADAL4849
ID ADAL4849 standard; cDNA; 1726 BP.
XX ADAL4849;
XX
XX 06-NOV-2003 (first entry)
XX Mouse interphotoreceptor matrix component, IPMC, 150 isoform D cDNA.
XX ss; gene; mouse; IPMC 150 isoform D; gene therapy;
XX interphotoreceptor matrix component; IPMC; ocular disorder;
XX macular degeneration; photoreceptor death; retinal detachment.
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 140..1540
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XX sig_peptide 140..199
XX /tag= a
XX /label= Signal_sequence
XX mat_peptide 200..1537
XX /tag= C
XX /label= Mature_IPMC_150_isoform_D
XX US2002160954-A1.
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XX 31-OCT-2002.
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XX 08-NOV-2001; 2001US-00007270.
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XX 29-OCT-1998; 98US-00183972.
XX 29-OCT-1999; 99US-00430195.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-238235/23.
XX P-PSDB; ADAL4850.
XX
```

PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.

XX  
 PS Claim 3; Page 43-44; 76pp; English.

CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding mouse  
 CC interphotoreceptor matrix component, IPMC, isoform D.

XX SQ Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;

# Alignment Scores:

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 DB: 9 Gaps: 9

US-10-007-270-2 (1-797) x ADA14849 (1-1726)

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 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro 40  
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 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
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 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
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 QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
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 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
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 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
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 QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 446 GAAGCCCTGTGTACCCACAGATGTTTCAGGATGTCCTGGGGCCATTCCTCCACTTCT 505  
 QY 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 Db 506 TCTGATGACACAGACCTCAGGAGATTTCTCAGTGTCAACCTCAAGGACATTCAAAAGGCC 565

QY 221 ThrThrGluArgGluThr -----GluPheAlaValLeuGluGluGln 234  
 Db 566 ACAACGAAGAGTATAACAGAACTATTTCAGTGTCTGAATCTTCA -----TCAGAGGAG 619  
 QY 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
 Db 620 AAGTGGAGTTCAGCATCTCTCTGCCAAACACAGAGTTCAGGCAGAGCTCACCACACTCT 679  
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 QY 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
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 QY 315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
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 QY 355 LeuLysArgLeuLysSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374  
 Db 977 CTCAAAAATCTCATACACTACTAGTAGGAGACCTGTCTTGTAGAGGAGAAATTT 1036  
 QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
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 QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
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 Db 1177 ----- 1177  
 QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474  
 Db 1177 ----- 1177  
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QY 575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSer 594
Db 1177 ----- 1177
QY 595 SerLeuGluTyrArgAlaLeuGluGlnPheThrGlnLeuLeuValProTyrLeuArg 614
Db 1177 ----- 1177
QY 615 SerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIle 634
Db 1178 -----AGAGAGGATCTGAGCTG 1195
QY 635 ValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHis 654
Db 1195 ----- 1195
QY 655 GlyValLeuGluAspPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSer 674
Db 1195 ----- 1195
QY 675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGly 694
Db 1196 -----CCTGCTGATCAGGCGGATCCCTGCAACTTCTAGACTGTGTC 1237
QY 695 GluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysPro 714
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QY 715 GlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThr 734
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Db 1355 AAGACTTGTGTGCGCGCCGAGAGACAGCAACTCCATGAGGCCAACAGATCACTCTACA 1414
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Db 1415 AACCAAGCTCAGGAACCTGGTGTAAAGAGCTA-----CGTCAGCAAAATTAAGGTAGTC 1468
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Db 1529 GAGGAAAT 1537
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Search completed: March 1, 2004, 21:06:43  
Job time : 922 secs



GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 18:13:35 ; Search time 7927 Seconds  
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4357.815 Million cell updates/sec

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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
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22: em.ov.\*  
23: em.pat.\*  
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26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	2759	67.0	3552	4	AB047844 Bos tauru
3	2548.5	61.9	3668	10	AF266478 Mus muscu
4	2546.5	61.9	2924	10	BC022970 Mus muscu
5	2543.5	61.8	2850	10	AB047843 Rattus no
6	2453	59.6	3675	10	AF229929 Mus muscu
7	1842.5	44.8	4953	5	AB070714 Gallus ga
8	933	22.7	3989	9	AF157624 Homo sapi
9	927	22.5	4165	9	AF173155 Homo sapi
10	911.5	22.1	4010	10	AY174061 Mus muscu
11	899	21.8	816	9	HSINPG33 Homo sapi
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13	899	21.8	132145	2	AL359817 Homo sapi
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15	886	21.5	4368	10	RUU76717 Rattus norv
16	885	21.5	555	9	AF047491 Macaca fa
17	875	21.3	6951	10	BC048863 Mus muscu
18	510.5	12.4	248573	2	AC096467 Rattus no
19	483.5	11.7	171412	2	AC120388 Mus muscu
20	408.5	9.9	537	9	HSINPG02 Homo sapi
21	408.5	9.9	132145	2	AL359817 Homo sapi
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23	406.5	9.9	444	9	HSINPG10 Homo sapi
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26	380	9.2	448	9	HSINPG14 Homo sapi
27	317	7.7	178064	2	AC023311 Homo sapi
28	317	7.7	178157	2	AC023311 Homo sapi
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32	315	7.7	270051	2	EX649245 Danio rer
33	310	7.5	422	9	HSINPG03 Homo sapi
34	308	7.5	222615	2	AC098280 Rattus no
35	264.5	6.4	60914	2	AC135246 Homo sapi
36	246	6.0	294851	2	EX649242 Danio rer
37	245	6.0	135646	2	AC119976 Mus muscu
38	245	6.0	171061	2	AC109266 Mus muscu
39	245	6.0	227553	2	AC116453 Mus muscu
40	243.5	5.9	159816	2	AC136044 Rattus no
41	241	5.9	1094	9	F271363812 Homo sapi
42	241	5.9	160042	2	AC027757 Homo sapi
43	234.5	5.7	377	9	HSINPG07 Homo sapi
44	195.5	4.7	219082	2	AC098274 Rattus no
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ALIGNMENTS

RESULT 1

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LOCUS      Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)
DEFINITION      mRNA, complete cds.
ACCESSION      AF047492
VERSION      AF047492.2      GI:6118565
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 3268)
AUTHORS      Kuehn, M.H. and Hageman, G.S.
TITLE      Expression and characterization of the IPM 150 gene (IMPG1)
PRODUCT      a novel human photoreceptor cell-associated
CHONDROITIN-SULFATE PROTEOGLYCAN
JOURNAL      Matrix Biol. 18 (5), 509-518 (1999)
MEDLINE      20068045
PubMed      10601738
REFERENCE      2 (bases 1 to 3268)
AUTHORS      Kuehn, M.H. and Hageman, G.S.
TITLE      Direct Submission
JOURNAL      Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PPF, Iowa City, IA
52240, USA
REFERENCE      3 (bases 1 to 3268)
AUTHORS      Kuehn, M.H. and Hageman, G.S.
TITLE      Direct Submission
JOURNAL      Submitted (26-OCT-1999) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PPF, Iowa City, IA
52240, USA
REMARK      Sequence update by submitter
COMMENT      On Oct 26, 1999 this sequence version replaced gi:2906231.
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## RESULT 2

AB047844 3552 bp mRNA linear MAM 30-AUG-2000  
 LOCUS Bos taurus mRNA for MLGAPC core protein, complete cds.  
 DEFINITION  
 AB047844  
 ACCESSION  
 VERSION AB047844.1 GI:9955919  
 KEYWORDS  
 SOURCE

## ORGANISM

Bos taurus (cow)  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.

## REFERENCE

1 (sites)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 AUTHORS  
 TITLE Isolation and characterization of mucinlike glycoprotein associated  
 with photoreceptor cells

## JOURNAL

Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)  
 MEDLINE  
 PUBMED 20391374  
 10937595

## REFERENCE

2 (bases 1 to 3552)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Direct Submission  
 Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University  
 Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
 Kagoshima 900-8520, Japan  
 E-mail:fuehara@med5.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
 Fax:81-99-265-4894

## FEATURES

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## ORIGIN



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RESULT 3
LOCUS AF266478 3668 bp mRNA linear ROD 18-AUG-2000
DEFINITION Mus musculus IPM 150 proteoglycan mRNA, complete cds.
ACCESSION AF266478
VERSION AF266478.1 GI:9844921
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3668)
Kuehn,M.H., Wietzecki,D.T. and Hageman,G.S.
Molecular characterization of the murine orthologue of the human
retinal proteoglycan IPM 150
Mol. Vis. 6 (2000) In press
2 (bases 1 to 3668)
Kuehn,M.H., Wietzecki,D.T. and Hageman,G.S.
Direct Submission
Submitted (10-MAY-2000) Ophthalmology, University of Iowa, 2501
Crosspark Rd., Coralville, IA 52241, USA
FEATURES
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## ORIGIN

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 DB: 10 Gaps: 9

US-10-007-270-2 (1-797) x AF266478 (1-3668)

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 ACCESSION BC022970  
 VERSION BC022970.1 GI:18606432  
 KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 2924)  
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Loquellano,N.A., Peters,G.J., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Zahery,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 2388257  
 12477932  
 REFERENCE 2 (bases 1 to 2924)  
 AUTHORS Strausberg,R.  
 Direct Submission  
 Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nananvati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 53 Row: k Column: 15  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 11528499.

## FEATURES

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## misc\_feature

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## ORIGIN

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 Percent Similarity: 75.12% Conservative: 79  
 Best Local Similarity: 65.35% Mismatches: 180  
 Query Match: 61.85% Indels: 21  
 DB: 10 Gaps: 9

US-10-007-270-2 (1-797) x BC022970 (1-2924)

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RESULT 5
AB047843
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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AB047843
AB047843.1 GI:9955917
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (sites)
Uehara, F., Ohba, N. and Ozawa, M.
Core Protein of rat Mucinlike Glycoprotein Associated with
Photoreceptor Cells
Published Only in DataBase (2000)
2 (bases 1 to 2850)
Uehara, F., Ohba, N. and Ozawa, M.
Direct Submission
Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University
Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,
Kagoshima 890-8520, Japan
(E-mail: fuehara@med5.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,
Fax:81-99-265-4894)
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## ORIGIN

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US-10-007-270-2 (1-797) x AB047843 (1-2850)

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AUTHORS Zako, M., Iwaki, M., Yoneda, M., Miyaiishi, O., Zhao, J., Suzuki, Y.,  
Takeuchi, M., Miyake, G., Ikagawa, H. and Kimata, K.  
TITLE Molecular Cloning and Characterization of Chick Sialoprotein  
Associated with Cones and Rods, a Developmentally Regulated  
Glycoprotein of Interphotoreceptor Matrix  
J. Biol. Chem. 277 (28), 25592-25600 (2002)  
JOURNAL  
PUBMED 11991949  
REFERENCE 2 (bases 1 to 4953)  
AUTHORS Zako, M. and Iwaki, M.  
TITLE Direct Submission  
JOURNAL Submitted (28-AUG-2001) Masahiro Zako, Aichi Medical University,  
Department of ophthalmology; Nagakute-cho, Aichi-gun, Aichi  
480-1195, Japan (E-mail:zako@aichi-med-u.ac.jp,  
Tel:81-52-264-4811 (ex.2181), Fax:81-561-63-7255)  
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Qy 753 ---SerGlu-AsnGlnAlaTyrLysThrSerValLysPheGlnAsnGlnGlnAsnAs 771
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RESULT 8
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LOCUS Homo sapiens Spacrcan mRNA, complete cds.
DEFINITION AF157624
ACCESSION AF157624
VERSION AF157624.1 GI:6467402
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3989)
AUTHORS Acharya,S., Foleta,V.C., Lee,J.W., Rayborn,M.E., Rodriguez,I.R.,
Young,W.S. III and Hollyfield,J.G.
TITLE SPACRCAN, a novel human interphotoreceptor matrix
hyaluronan-binding proteoglycan synthesized by photoreceptors and
pinealocytes
JOURNAL J. Biol. Chem. 275 (10), 6945-6955 (2000)
MEDLINE 20167166
PUBMED 10702256
REFERENCE 2 (bases 1 to 3989)
AUTHORS Foleta,V.C. and Young,W.S.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1999) SNGE, NIMH, 36 Convent Dr, MSC 4068,
Bethesda, MD 20892-4068, USA
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DEFINITION mRNA, complete cds.
ACCESSION AF173155
VERSION AF173155.1 GI:6318679
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4165)
AUTHORS Kuehn,M.H. and Hageman,G.S.
TITLE Molecular characterization and genomic mapping of human IPM 200, a
second member of a novel family of proteoglycans
JOURNAL Mol. Cell Biol. Res. Commun. 2 (2), 103-110 (1999)
MEDLINE 20391216
PUBMED 10542133
REFERENCE 2 (bases 1 to 4165)
AUTHORS Kuehn,M.H. and Hageman,G.S.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Ophthalmology, University of Iowa, 2501
Crosespark Rd., Coralville, IA 52241, USA
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## ORIGIN

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 Best Local Similarity: 26.68% Mismatches: 267  
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## RESULT 10

AY174061

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .4010

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/mol\_type="mRNA"

/db\_xref="taxon:10090"

/chromosome="16"

/note="specifically expressed in retina and pineal gland;

detectable as early as E15"

226..3609

/note="SPACKCAN; similar to Rattus norvegicus PGI0.2 and

Homo sapiens IPM200; retinal-specific protein present in

the interphotoreceptor matrix"

/codon\_start=1

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proteoglycan"

/protein\_id="AA021221.1"

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## ORIGIN

Alignment Scores:  
 Pred. No.: 8,77e-54 Length: 4010  
 Score: 911.50 Matches: 279  
 Percent Similarity: 42.43% Conservative: 136  
 Best Local Similarity: 28.53% Mismatches: 272  
 Query Match: 22.14% Indels: 291  
 DB: 10 Gaps: 35

US-10-007-270-2 (1-797) x AY174061 (1-4010)

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 Qy 51 MetTyrLysMetSer-----ThrMetArgArgIlePheAspLeuAlaLysHis--- 66  
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 Db 415 AGSAGGTGCTGCTTGAAGAGGGCGGATCTATTCTTGTCCCAATGGAGTAAATTTGC 474  
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 Qy 102 CysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThrGly 121  
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 Qy 122 GluTyrGluAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIleGly 141  
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 Qy 142 LysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIle----- 158  
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 Qy 159 LysGlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGlu 178  
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 Qy 196 ProPhePro-----LeuThrProAspAspThrLeuLeuAsn 207  
 Db 823 TCCTATCCAGGGTTGGCTTCGAGAGAGCGCAGCGGTCAACCCGAGAGAGTATCAGCAAT 882  
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Qy 228 PheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
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 Qy 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnIleLeuAlaGlyLysSerGln 267  
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 Qy 288 PheArgProLysLysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
 Db 1090 TTCAGGCCCCGGAGGAAATGACAGTGGATAGATTTCACCTATGCAGTTACC----- 1143  
 Qy 308 PheLysArgHisSerAlaGluAlaLysSerProAlaSer---AspLeuLeuSerPheAsp 326  
 Db 1144 -----TTCATGGCGAAGCCATCAGCAATACCACCTGGGACCTCTAAGCCTTCAC 1194  
 Qy 327 SerAsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnPro 346  
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 Qy 347 GluIleTyrLeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeuGluGlu 366  
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 Qy 401 ValIleThrGluAspAlaThrLeuSerProGlu----- 411  
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 Qy 412 -----LeuProValGlu----- 416  
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 Qy 417 -----ProGlnLeuGlu-----Thr 421  
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 Qy 439 MetAlaSerThr-----SerLeuSerGluAlaPro----- 448  
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Db 2014 TTTTCAAAACACACTTCAGATGTAACAGACATTTGATTTCTTACTCACTTACCAACACACC 2073
QY 475 LeuValPro---GlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
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QY 494 LeuGlyIleSerHisProProAlaSerSerAsp-----AspSerArgSerSerAla 510
Db 2134 GAAGATATGTCATACAGATCATCCACTCACAAGAACTTGACAGTGCAGTTCAGTG 2193
QY 511 GlyGlyGluAspMet-----515
Db 2194 TCAAGGCCAGATATGAGCGCTGTGTGGACCATGTTGCCAGATCAGATACAGTTCGGACA 2253
QY 516 -----ValArgHisLeuAspGluMetAspLeuSerAspThrPro-----528
Db 2254 AGAATCTTCTCTAGGAAATGTCAGAGACACATTTGGCAAGTACACAGAGAGACT 2313
QY 529 -----AlaProSerGluValPro-----534
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QY 535 -----GluLeuSerGlnTyrValSerVal-----542
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QY 543 -----ProAsp 544
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QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564
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Db 2545 GCTCTGCCCAAAAGAGAGGTCTTGTAGTCACACCCAGACTGCAGGACATGTTGTGT 2604
QY 576 PhePheSerLeuArgValAlaAlaSerMetAlaPheSerAsnAspLeuPheAsnLysSerSer 595
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QY 596 LeuGluTyrArgAlaLeuGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSer 615
Db 2665 TTGGATATAAGCCCTGGAACAAAGATTTCTTAGAACTGCTGGTTCCTATCTCCAGTCA 2724
QY 616 AsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleVal 635
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QY 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715
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RESULT 11
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DEFINITION Homo sapiens interphotoreceptor matrix gene (IPM150), exon 13.
ACCESSION AF017772
VERSION AF017772.1 GI:3800727
KEYWORDS
SEGMENT
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 816)
AUTHORS Felber, U., Gehrig, A., Sauer, C.G., Marquardt, A., Kohler, M.,
Schmid, M. and Weber, B.H.
TITLE Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
JOURNAL 98358139
MEDLINE 9891169
PUBMED
REFERENCE 2 (bases 1 to 816)
AUTHORS Gehrig, A., Felber, U., Kessel, R., Hunt, D.M., Maumensee-Hussels, I.E.
and Weber, B.H.F.
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bifocal choroideretal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRI)
Unpublished
JOURNAL
AUTHORS
AUTHORS Felber, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
TITLE Direct Submission
Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
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exon

ORIGIN

Alignment Scores:
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Best Local Similarity: 59.44% Mismatches: 0
Query Match: 21.84% Indels: 0
DB: 9 Gaps: 0

US-10-007-270-2 (1-797) x HSIIMP13 (1-816)
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QY 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490
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 QY 591 PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
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RESULT 12  
 AL392166/c  
 LOCUS  
 DEFINITION Human DNA sequence from clone RP11-758J17 on chromosome 6, complete  
 sequence.  
 ACCESSION AL392166  
 VERSION  
 KEYWORDS HTG.  
 SOURCE AL392166.19 GI:13396652  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (Bases 1 to 90766)

REFERENCE  
 AUTHORS Clark.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk

COMMENT  
 On Mar 20, 2001 this sequence version replaced gi:13234983.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; Swi,  
 SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP  
 database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
 This sequence was generated from part of bacterial clone contigs of human  
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr6>  
 RP11-758J17 is from the library RP11-11.3 constructed by the group  
 of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP11-758J17. It may be shorter because we sequence overlapping  
 sections only once, except for a 100 base overlap.

The true left end of clone RP11-62L18 is at 24664 in this sequence.  
 The true left end of clone RP11-453C2 is at 90667 in this sequence.  
 The true right end of clone RP3-472A9 is at 100 in this sequence.

## FEATURES

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----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA505B21
----- Summary Statistics
Assembly program: XAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 117761 bases at least Q40
Consensus quality: 123343 bases at least Q30
Consensus quality: 126505 bases at least Q20
Insert size: 129645; sum-of-contigs
Insert size: 166195; 8.3% error; agarose-fp
Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality
coverage: 2.65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 8912: contig of 8912 bp in length
* 8913 9012: gap of 100 bp
* 12665 12765: contig of 3653 bp in length
* 12666 12765: gap of 100 bp
* 12766 16825: contig of 4060 bp in length
* 16826 16925: gap of 100 bp
* 16926 22958: contig of 6033 bp in length
* 22959 23058: gap of 100 bp
* 23059 25080: contig of 2022 bp in length
* 25081 25180: gap of 100 bp
* 25181 27272: contig of 2092 bp in length
* 27273 27372: gap of 100 bp
* 27373 40754: contig of 13382 bp in length
* 40755 40854: gap of 100 bp
* 40855 45147: contig of 4293 bp in length
* 45148 45247: gap of 100 bp
* 45248 48493: contig of 3246 bp in length
* 48494 48593: gap of 100 bp
* 48594 52881: contig of 4288 bp in length
* 52882 52981: gap of 100 bp
* 52982 57112: contig of 4131 bp in length
* 57113 57122: gap of 100 bp
* 57213 60637: contig of 3425 bp in length
* 60638 60737: gap of 100 bp
* 60738 62745: contig of 2008 bp in length
* 62746 62845: gap of 100 bp
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* 70685 70784: gap of 100 bp
* 70785 74560: contig of 3776 bp in length
* 74561 74660: gap of 100 bp
* 74661 77242: contig of 2582 bp in length
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* 77343 81104: contig of 3762 bp in length
* 81105 81204: gap of 100 bp
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* 83751 83850: gap of 100 bp
* 83851 92862: contig of 9112 bp in length
* 92863 93062: gap of 100 bp
* 93063 106092: contig of 13030 bp in length
* 106093 106192: gap of 100 bp
* 106193 110395: contig of 4803 bp in length
* 110396 111025: gap of 100 bp
* 111026 114862: contig of 3787 bp in length
* 114863 114963: gap of 100 bp
* 114963 118827: contig of 3865 bp in length
* 118828 118927: gap of 100 bp

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misc_feature      118928..124084
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ORIGIN
Alignment Scores:
Pred. No.:      8.18e-51      Length:      132145
Score:          899.00      Matches:      178
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.44%      Mismatches: 0
Query Match:    21.84%      Indels:      0
DB:             2          Gaps:          0

US-10-007-270-2 (1-797) x AL1539817 (1-132145)
Qy 431 AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProProphe 450
Db 14959 GACACTTCTGGTCTCCACCTGCTATGCGCTTACCTCCCTGTGTCAGAGCTCCACCTTTC 15018
Qy 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470
Db 15019 TTTATGGCATCAGCATCTTCTCTCTGACTGATCAAGGACCACACATCAATGGCCACT 15078
Qy 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490
Db 15079 GACCAGCAATGCTAGTACACAGGCTCACCATCCACCAGTGTATTCTGCATCAGC 15138
Qy 491 GlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerArgSerAla 510
Db 15139 CAATGGCTCTGGGAATTTCCATATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCA 15198
Qy 511 GlyGlyLeuAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaPro 530
Db 15199 GTTGGCGAAGATATGTCACACACCTAGATGAATGGAATGCTGTGACACTCTCTGCCCA 15258
Qy 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550
Db 15259 TCTGAGTACACAGCTCAGCAATATGTTCTGTCCAGATCATTTCTTGAGGATACC 15318
Qy 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGly 570
Db 15319 ACTCTGTCTCAGCTTTACAGTATATCACCACCTAGTTCATGACCATGCCCCCAAGGCG 15378
Qy 571 ArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeu 590
Db 15379 CGAGAGCTGTAGTGTCTTTCAGTCTCGGTGTTGCTAACATGGCTTCTCCAGACCTG 15438
Qy 591 PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
Db 15439 TTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGGTG 15495

RESULT 14
AL157379/c      160719 bp      DNA      linear      HTG 11-SEP-2001
LOCUS          Homo sapiens chromosome 6 clone RPI-62L18.
DEFINITION     AL157379
ACCESSION      AL157379
VERSION        AL157379.14 GI:15590763
KEYWORDS       HTG; HTGS PHASE2; HTGS_CANCELLED.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1

```

# AUTHORS TITLE

Wall, M.  
Direct Submission  
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Sep 12, 2001 this sequence version replaced gi:11991356.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: dj62L18  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 160382 bases at least Q40  
Consensus quality: 160493 bases at least Q30  
Consensus quality: 160578 bases at least Q20  
Insert size: 160719; sum-of-contigs  
Insert size: 158939; 9.3% error; agarose-fp  
Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
coverage: 8.41x in Q20 bases; agarose-fp

## COMMENT

\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

## FEATURES

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vector\_side:right

### misc\_feature

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## ORIGIN

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Pred. No.: 1.07e-50 Length: 160719  
Score: 899.00 Matches: 178  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.44% Mismatches: 0  
Query Match: 21.84% Indels: 0  
DB: 2 Gaps: 0

US-10-007-270-2 (1-797) x AL157379 (1-160719)

Qy 431 AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProProphe 450  
Db 7762 GACACTTCTGGTCTCCACCTGCTATGCGCTTACCTCCCTGTGTCAGAGCTCCACCTTTC 7703  
Qy 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
Db 7702 TTTATGGCATCAGCATCTTCTCTGACTGATCAAGGACCACACATCAATGGCCACT 7643  
Qy 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490  
Db 7642 GACCAGCAATGCTAGTACACAGGCTCACCATCCCACTGATTTCTGCAATCAGC 7593  
Qy 491 GlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerArgSerAla 510  
Db 7592 CAATGGCTCTGGGAATTTCCATATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCA 7523  
Qy 511 GlyGlyLeuAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaPro 530

Db 7522 GGTGGCAAGATATGGTCAGACACCTAGATGAAATGATCTGTCTGACACTCTCTGCCCCA 7463

Qy 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550  
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Db 7462 TCTGAGGTACAGAGCTCAGCAATATGTTCTGTGCCAGATCATTTCTTGGAGGATACC 7403  
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Qy 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGly 570  
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Db 7402 ACTCCTGTCTCAGCTTTACAGTATATCACCACCTAGTTCTATGACCATTTGCCCAAGGCG 7343  
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Qy 571 ArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeu 590  
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Db 7342 CGAGAGCTGTAGTGTCTTTCAGTCTCGTGTGCTTAACATGGCTTCTTCCACAGCACTG 7283  
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Qy 591 PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
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Db 7282 TTCACACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACATTCACACAGCTGGTG 7226  
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RESULT 15

LOCUS RNU76717 4368 bp mRNA linear ROD 13-NOV-1996

DEFINITION Rattus norvegicus PG10.2 mRNA, complete cds.

ACCESSION U76717

VERSION U76717.1 GI:1667596

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 4368)  
Wang,X., Brownstein,M.J. and Young,W.S. III.  
Sequence analysis of PG10.2, a gene expressed in the pineal gland  
and the outer nuclear layer of the retina  
Brain Res. Mol. Brain Res. 41 (1-2), 269-278 (1996)  
97038366

REFERENCE 2 (bases 1 to 4368)  
Wang,X., Brownstein,M.J. and Young,W.S.  
Direct Submission  
Submitted (30-OCT-1996) LCMR, NIMH, 36 Convent Drive, MSC 4068,  
Bethesda, MD 20892-4068, USA  
9883960

FEATURES  
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## ORIGIN

## Alignment Scores:

Pred. No.: 5,94e-52 Length: 4368  
Score: 886.00 Matches: 281  
Percent Similarity: 37.74% Conservative: 127  
Best Local Similarity: 25.99% Mismatches: 265  
Query Match: 21.52% Indels: 408  
DB: 10 Gaps: 33

US-10-007-270-2 (1-797) x RNU76717 (1-4368)

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Db 316 GAGTCAACAGACCTTTCCCTCCCTACCAGGAAGAGACAGCTTTTGGATGCCACAGAG--- 372  
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Qy 51 MetTyrLysMetSerThrMetArgIlePheAspLeuAlaLysHisArgThrLysArg 70  
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Db 373 -----ACTGGAGAGGAGG---TGGCCGCTT-----AGAAGCGGACGA 405  
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Qy 71 SerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeu 90  
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Db 406 TCTATTCTGTTCCTCCAAATGGAGTAAAGATTTCCTCCCTGACACACTGTTGCAGAGCGTGTG 465  
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Qy 91 AspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTTPGluAlaTyr 110  
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Db 466 GCAAACCATGTGAAGTATTTTAAAGCCGAGTGTGCCAGGAGCCATCTGGAGACCTTC 525  
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Qy 111 ArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTTPValSerIleCys 130  
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Db 526 AGGACATTTTGGGACCGACTTCTCTGGCGTGAGGAATATCAATCTGATGAACCTATGT 585  
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Qy 131 GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSerGlnGluHis 150  
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Db 586 GAGGATGGAGTCAACAGTGTATTGAAATGGGACCCAGTATTAGTCAATCTGTGGAACAC 645  
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Qy 151 LeuAspLeuLeuGlnGlnArgIle-----LysGlnArgSerPheProAspArgLys 167  
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Db 646 AGACACTTATCATCGAGAAATTCACATACACAAAGGAGCTGAGAGCGCTCTGCAAG 705  
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Qy 168 Asp-----GluIleSerAlaGluLysThrLeuGlyGluProGlyGluThr 182  
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Db 706 GATCAGCGCTGTGGACCTGAGTGTCTCTCAGTCTCCTATTTGCGGAG----- 753  
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Qy 183 IleValIleSerThrAspValAlaAsnValSerLeuGlyProPhePro----- 198  
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Db 754 -----ACCTCAACATTGGGAGGTGTCTTCCAGTCTTCTTATCCAGGGCGGCTCA 807  
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Qy 199 -----LeuThrProAspThrLeuLeuAsnGluIleLeuAspAsnThrLeu 214  
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Db 808 GAGAGAAGCGCGGATCACCACAGAGAGATATCAGCAATGAAAT-----GAG 855  
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Qy 215 AsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGln 234  
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Db 856 AATGTGACAGAGCGCCACACCCGCA-----GCTGCTGAACAG 894  
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Qy 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
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Db 1015 ACAGGTTACCTGGCTACAGGGCATCCATGTTCTGATTTTCAGTCTCCAAAGGAAAT 1074  
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Qy 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
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1075 GGCAGTGGGATAGATGTTCACTATGCGATTACT-:::|||||:::---TTCAACGGCGAG 1119  
QY 315 AlaLysSerProLaseR---AspLeuLeuSerPheAspSerAsnLysIleGluSerGlu 333  
D 1120 GCCATCAGCAATACCACTGGACCTTCATAAGCCTTCACTCCCAACAAGGTGGAGAAC-- 1176  
QY 334 GluValTyHicGlyThrMetGluGluAspLysGlnProGluIleTyLeuThrAlaThr 353  
D 1177 ---CATGGCCTTGTAGAGCTGGATGATATAAACCCACGGCGCTCTATACGATCAGT 1227  
QY 354 AspLeuLysArgLeuLysSerLysAlaLeuGlu---:::|||||:::--- 364  
D 1228 AACTTCAGAGATTATATCGCTGAGACACTGACCCAGAGAACTTTTAATGGGAATTTCTTCT 1287  
QY 364 ---:::|||||:::--- 364  
D 1288 TTGAATCCAGATCCCAAGTCTCTCCAGCTTATCAATGTGAGAGGATTTCTGCTCCCCCAA 1347  
QY 365 ---GluGluGlnSerLeuAspValGlyThrIleGlnPhe 376  
D 1348 ACGGAGAAATAGTTTGGAAACACCCAAAGTTCAGTCTTCAGGTGACAACTCTCTATT 1407  
QY 377 ThrAspGluLeu---:::|||||:::--- 380  
D 1408 CTGGATAATACCTGCAAGCTGAATGGCTCTCAGCAGATGAATCCATCACCACCACCACC 1467  
QY 381 ---:::|||||:::---AlaGlySerLeuProAlaPheGlyProAsp 390  
D 1468 ACCACCACTATTTCACCAATTTGGTTTCACTCCGGTCTCCCTCAGCCACTGGCAGGGAA 1527  
QY 391 ThrGlnSerGlu---:::|||||:::---LeuProThr 397  
D 1528 CTCCATTGAGAAAGTACTTTGGTGACATAGTGTCTACACCAAGTAGCTTCTCCCTCG 1587  
QY 398 SerPhe---:::|||||:::--- 399  
D 1588 AAGGTGGTCTCAGTTCCTCCCGAGAGGTTTGGGGGTAGCAGCTTGACTTCTTCAATCT 1647  
QY 400 ---AlaValIleThrGluAspAlaThrLeuSerProGlu---:::|||||:::--- 411  
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QY 411 ---:::|||||:::--- 411  
D 1708 TCTTCCATATTAGAAGACGACACACAGAGAATCAGAAGATGTTTCTATTGATGATTG 1767  
QY 412 ---:::|||||:::---LeuProValGlu--- 416  
D 1768 CCTTCAGCTCATTAATTCACCTGTGCCAAAGAAACAGTACCACCCATGGAAGACTCT 1827  
QY 416 ---:::|||||:::--- 416  
D 1828 GACATGATTCTCTGACATCTCCACACATCTGACCTCTTCTGTGTPATAGAGACCTTGCT 1887  
QY 417 ProGlnLeuGluThrValAspGlyAlaGluHis---:::|||||:::--- 427  
D 1888 AAAGACATAACGACACCTTCTGGCTTGGACTCCTTTGGCTTCCAGAGTCTCAGACAAGTTG 1947  
QY 428 ---GlyLeuProAspThrSer---:::|||||:::--- 433  
D 1948 GACGTGAGCCCATGGTTTCCAGACACCTCTGTGGAAAAGAGTTCATTTTGAAGTGGC 2007  
QY 434 ---:::|||||:::---TyrSerProAla 438  
D 2008 TTGGGCTCTGGGTCTGGGAAAATGTTCGATGTGATTGTTGGCCATGGAGTGAGACTTCA 2067  
QY 439 MetAlaSerThrSer---:::|||||:::--- 443  
D 2068 TTAGAGAGACCACCTGAACCCCTGTCAAAGTCATGGTCTGAAGACGAGATACACTATTA 2127  
QY 443 ---:::|||||:::--- 443

2128 CCAACTGAGAGTATAGAAAAATTACATATGTTATTTTCACAGAACAAATGATTGAACCTTCA 2187  
QY 443 ---:::|||||:::--- 443  
D 2188 GCACATAGATATGGAGATGGACCCATATATTTTACAGAGGAAGAAATCCCATGTTAGATCT 2247  
QY 443 ---:::|||||:::--- 443  
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D 2368 ---ACTATAGCAAAACACTGCTTCCACCAAGGAACACAGATGAGGTG 2409  
QY 473 ---ThrMetLeuValProGlyLeuThr---:::|||||:::--- 480  
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QY 481 ---:::|||||:::---IleProThrSer 484  
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QY 498 HisPro---:::|||||:::---ProAlaSerSer 503  
D 2590 ACACGAGAGCGCTGACAGACTCTGGTTGAAGCCCTCCATGACACAGCCGCTGAATTG 2649  
QY 504 AspAspSerArgSerAlaGlyGlyGluAsp---MetValArgHisLeuAsp 520  
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QY 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu--- 538  
D 2710 TCATTAGAACTAGACAGGTAGCCAGGATTAATCAGCTGAGCTGAGTAAACCCAGAACAA 2769  
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QY 573 LeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsn 592  
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QY 593 LysSerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyr 612  
D 2947 AAAAATCTTTGGAGTATAAAGCCCTGGAGCAAGATTTCTTAGAACTGCTGTTCCCTAT 3006  
QY 613 LeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySer 632  
D 3007 CTCAGTCMAATCTGTGCGGTTCCAGAACTTAGAGATCTCTGAACTTCAGAAATGGCAGC 3066  
QY 633 ValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAla 652  
D 3067 ATTGTGTGAACAGCAGGAGTGAAGTTCCGCGAGTCTGCTCCTCCTTAATGTCAACACGCC 3126  
QY 653 ValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIle 672  
D 3127 ATATATGATCTTGAAGACTTTTGTACCCCGCTTACCAACCAACCACTTGGATATT 3186  
QY 673 AspSerTySerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAla 692  
D 3187 GATAAGTACTCCCTGGATGGAATCAGGTGATGACGCCAACCCCTTGCAAGTTTCAGGCC 3246

